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STI	C-E	3io	tec	h/C	her	nLib

From: Sent: To: Subject:

Chan, Christina

Thursday, January 24, 2002 2:49 PM Kemmerer, Elizabeth; STIC-Biotech/ChemLib

RE: rush seq search req

Flease rush. Thanks Chris

-----Original Message-----

From:

Kemmerer, Elizabeth

Sent:

Thursday, January 24, 2002 2:27 PM

To:

Chan, Christina

Subject:

rush seq search req

Hi Christina-

Please approve the following for a due amended:

STIC:

Please do a regular and interferences search of SEQ ID NO: 26 (full length) and an oligo search of 30 contiguous amino acids of SEQ ID NO: 26 for 08/741095

Thanks,

Elizabeth (Betsy) Kemmerer Art Unit 1646 308-2673 CM1-10B17 Mailbox: 10C01

Searcher:	
Phone:	
Location:	
Date Picked Up: 124/182	
Date Completed: 1/125/107	
Searcher Prep/Review:	
Clerical:	
Online time:	

TYPE OF SEARCH:
NA Sequences:
AA Sequences:
Structures:
Bibliographic:
Litigation:
Full text:
Patent Family:

Other:

VENDOR/COST(v	where applic.)
DIALOG:	
Questel/Orbit: _	
DRLink:	
Lexis/Nexis:	
Sequence Sys.:	08
WWW/Internet:	
Other (specify):	

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Minimum DB
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Copyright (c) 1993 - 2000 Compugen Ltd.
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AAJ01819	AAJ01758	AAJ01463	AAJ01152	AAJ00288	AAJ00162	AAB98703	AAY47926	AAJ01702	AAJ01151	AAY79208	SUMMARIES
Hepatitis C virus	Hepatitis C virus	C	Hepatitis C virus	a	Hepatitis C virus	Cytotoxic T Lympho	Immunogenic peptid	Hepatitis C virus	Hepatitis C virus	sHVEM1-Fc fusion N	Description

ALIGNMENTS

RESULT AAY79208

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sHVEM1-Fc fusion N-terminal peptide

19-JUN-2000 (first entry)

AAY79208;

AAY79208 standard; Peptide;

10 A

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sHVEM-1; soluble herpesvirus entry mediator-1; TANGO-69-receptor; tumour necrosis factor receptor; human; herpes simplex virus; infection; cancer; inflammation; autoimmune disorder; therapy;
                                                                    03-SEP-1998;
29-JUN-1999;
                      WPI; 2000-256981/22.
                                      Busfield
                                                                                             03-SEP-1999;
                                                                                                                            WO200014230-A1
                                                                                                                                                            diagnosis.
                                                                                                             16-MAR-2000.
                                                                                                                                           Homo sapiens.
                                                     (MILL-) MILLENNIUM BIOTHERAPEUTICS INC
                                                                     98US-0146950.
99US-0342767.
                                                                                             99WO-US20180
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New nucleic acid molecule encoding herpes virus entry mediator (HVEM), either in the soluble or membrane bound form, is useful in screening

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RESULT
AAJ01151
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Best Local
Sequence
                     The present invention describes a composition comprising a prepared hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121. These are derived from HCV HLA-binding motifs. They are useful in vaccines for the prevention and treatment of HCV infection in humans. The present sequence is an epitope used in the disclosure of the invention.
                                                                                                                                                                        Baker
                                                                                                                                                                                    Sette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-terminus of a mature human TANGO-69-receptor:IgG1 Fc fusion protein. The fusion protein was expressed in HEK 293° cells that had been transfected with a vector carrying a gene fusion composed of the human TANGO-69-receptor (sHVEM1, see AAX94195) coding sequence and DNA encoding the Fc domain of human IgG1. sHVEM1 (see also AAY79204) is a novel soluble form of membrane-bound herpesvirus entry
                                                                                                Disclosure;
                                                                                                                                                                                                            (EPIM-) EPIMMUNE INC
                                                                                                                                                                                                                                                           19-JUL-2000; 2000WO-US19774.
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                                                                                                                                                                                                                                                                                                                                   Hepatitis C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAJ01151 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mediator (mHVEM). DNA encoding HVEMs, HVEM proteins and HVEM antibodies can be used in screening and detection assays. HVEM proteins can also be used for regulation of cell proliferation, cell differentiation, cell survival, inflammation mast cell
                                                                                                                                                                                                                                   19-JUL-1999;
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                                                                                                                                                                       Sidney J,
Celis E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          herpes simplex virus infection and/or proliferation,
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                                                                                                                                                                                                                                                                                                                                   virus
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Best Local 9
Human leukocyte antigen; binding; immunogenic; glycoprotein; immune response; T cell activation; major histocompatibility
                                                                                                                                                                                                                                         The present invention describes a composition comprising a prepared hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121. These are derived from HCV HLA-binding motifs. They are useful in vaccines for the prevention and treatment of HCV infection in humans. The present sequence is an epitope used in the disclosure of the invention.
                                                                                                                                                                                                                                                                                                                       .A new
                                                                  AAY47926;
                                                                                    AAY47926 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                        WPI; 2001-308046/32.
                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                   Disclosure; Page 143; 214pp;
                                                                                                                                                                                                                                                                                                                                                            Baker
                                                                                                                                                                                                                                                                                                                                                                    Sette
                           Immunogenic peptide having a human leukocyte antigen binding motif #2537
                                                                                                                                                                                                                                                                                                                                                                                                          19-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hepatitis C virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hepatitis C virus;
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Celis E,
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MHC; HLA; complex;
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                                                                                                                                      AAB98703
                                                                                                                                                    RESULT
                                                                                                                                                                                                                                                                                                                                                                                                    having a human major histocompatibility complex (MHC) Class I (also cknown as human leukocyte antigen (HLA) binding motif. The immunogenic peptides can bind to a specific HLA allele (i.e. HLA-A subtypes CHLA-A2.1, A1, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell response against the antigen from which the peptide is derived. Cytotoxic T lymphocytes (CTLS) which destroy antigen-bearing cells are normally induced by an antigen in the form of a peptide fragment bound to a HLA molecule, rather than the intact foreign antigen itself, and are particularly important in tumour rejection and in fighting viral infections. The peptides are therefore useful therapeutically to treat or prevent viral infections and cancers in mammals (especially humans) c.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma. They can be administered as vaccines to elicit an immune response in individuals susceptible or otherwise at risk of viral infection or
                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 6
Cytotoxic T lymphocyte epitopic peptide p214K9; hepatitis C virus; NS3; NS4; NS5a; NS5b; p214K9; immune response; CTL; HCV; hepatitis C virus infection.
                                               Cytotoxic T
                                                                          02-AUG-2001
                                                                                                   AAB98703
                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                  cancer, or used to treat chronic or acute conditions. They are also useful diagnostically, and can be used to induce a cytotoxic T cell response, by contacting a cytotoxic T cell with the peptide e.g. to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and
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                                                                                                                         AAB98703 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (EPIM-) EPIMMUNE INC
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                                                                                                                                                                                                                                                                                                                               polynucleotides enco
                                                                                                                                                                                                                                                                                                                                                       produce CTLs ex vivo for infusion back into a patient.
                                                                                                                                                                                                                145 SPGQRV 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to AAY48214 represent specifically claimed immunogenic peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Page 128; 150pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immunisation.
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                                                                                                                                                                                                                                                                                                         ٥
                                               Lymphocyte
                                                                                                                                                                                                                                           Conservative
                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                               encoding the immunogenic peptides are also useful and for immunisation as above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sidney J,
                                                                                                                                                                                                                                        2.1%; Score 6; DB 20; L
100.0%; Pred. No. 4.3e+05;
tive 0; Mismatches 0;
                                               epitopic peptide p214K9 from hepatitis C virus
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                                                                                                                                                                                                                                                                Length 9;
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Вb
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                either an NS3, NS4 and NS5a polypeptide of HCV, or an NS3, NS4, NS5a and NS5a polypeptide of HCV, or an NS3, NS4, NS5a and NS5b polypeptide of an HCV. The HCV polypeptides are particularly useful for stimulating cell-mediated immune responses, e.g. activating HCV-specific T cells. The fusion protein is useful for generating an immune response against HCV in a mammal, particularly a cytotoxic T lymphocyte (CTL) response for either therapeutic or prophylactic treatment against HCV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immunisation with plasmid or naked DNA encoding an NS3NS4NS5a fusion protein will activate CD8+ cells which recognise and lyse target cells displaying an NS5a epitope. The present sequence was useful in the production of the invention which includes fusion proteins comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents cytotoxic T lymphocyte epitopic peptide p214K9 which comes from hepatitis C virus NS5a protein (HCV-NS5a), this sequence was used in an experiment of the invention to show that
19-JUL-1999;
                                                                                                                                                                                                                                      antiviral.
                                                                                                                                                                                                                                                                                                      Hepatitis C virus epitope #153
                                                                                                                                                                                                                                                                                                                                                     02-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                       AAJ00162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAJ00162 standard; Peptide; 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hepatitis C virus (HCV) polypeptides and fusion proteins, useful for stimulating cell-mediated immune responses, particularly for therapeutic or prophylactic treatment against HCV infection hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-OCT-1999;
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                                            19-JUL-2000; 2000WO-US19774.
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                                                                                                                                                                                    Hepatitis C virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46 EYPVGS 51
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| 2 eypvgs 7
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ilarity 100.0%;
Conservative
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99US-0357737
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                                                                                                                                                                                                                                                            immunogen; HLA-binding motif;
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Best Local :
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Baker DM,
                The present invention describes a composition comprising a prepared hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121. These are derived from HCV HIAD-binding motifs. They are useful in vaccines for the prevention and treatment of HCV infection in humans. The present sequence is an epitope used in the disclosure of the invention.
                                                                                                                   WPI;
Sequence
                                                                             Disclosure;
                                                                                                                                                                                                         19-JUL-2000;
                                                                                                                                                                                                                                               WO200121189-A1
                                                                                                                                                                                                                                                                 Hepatitis C virus
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                                                                                                                                                                                                                                                                                                                  Hepatitis C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A new composition useful as a vaccines
                                                                                                                                                                   (EPIM-)
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nes 6; Conserv
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Celis E,
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Celis E,
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                                                                            Page 107;
                                                                                                                                                                                                                                                                                                                  virus
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100.0%;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                     WPI;
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Baker
                          Hepatitis C
                                             02-JUL-2001
                                                                AAJ01463;
                                                                                   AAJ01463
                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                                                  A new
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Celis E,
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100.0%;
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antiviral Hepatitis C

virus;

HCV; epitope;

vaccine;

immunogen;

HLA-binding

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Best Local S
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Baker DM,
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Baker DM,
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Disclosure; Page 144; 214pp; English
                   A new composition useful as a vaccines against hepatitis
                                      WPI; 2001-308046/32
                                                                                                      19-JUL-1999;
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                                                                                                                                                               WO200121189-A1
                                                                                                                                                                                 Hepatitis C virus.
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Celis E,
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Celis E,
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llarity 100.0%; Pred. No.
Conservative 0; Mismatci
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                                                        Southwood S, Livi
Kubo RT, Grey HM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Southwood S, Livi
Kubo RT, Grey HM;
                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                              vaccine;
                                                                  Livingston BD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Livingston
                                                                                                                                                                                                                                                                                                                                                                                      DB 22; L
                                                                                                                                                                                                             immunogen; HLA-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BD,
                                                                                                                                                                                                                                                                                                                                                                             0,
                                                                                                                                                                                                                                                                                                                                                                                              Length 9;
                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                  Chesnut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chesnut
                    C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C
                                                                  ₽,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70,
                    virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                       in humans. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        virus
                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                             Gaps
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RESULT AAJ02614

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RESULT 1
AAJ01819
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                                            Query Match
Best Local S
Matches 6
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                Sette A,
Baker DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes a composition comprising a prepared hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121. These are derived from HCV HLA-binding motifs. They are useful in vaccines for the prevention and treatment of HCV infection in humans. The present sequence is an epitope used in the disclosure of the invention.
                                                                                                                       The present invention describes a composition comprising a prepared hepatitis C virus (HCV) epitope such as those given in AAJ04121. These are derived from HCV HLA-binding motifs. They are useful in vaccines for the prevention and treatment of HCV infection in humans. The present sequence is an epitope used in the disclosure of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Hepatitis C virus; HCV; epitope;
antiviral.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-JUL-2001
                                                                                                   Sequence
                                                                                                                                                                                             Disclosure; Page 145;
                                                                                                                                                                                                                    A new
                                                                                                                                                                                                                                         WPI; 2001-308046/32.
                                                                                                                                                                                                                                                                                                                                                                                            WO200121189-A1
                                                                                                                                                                                                                                                                                                                                                                                                                 Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hepatitis C virus epitope #1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAJ01819;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAJ01819 standard; Peptide; 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                          19-JUL-1999;
                                                                                                                                                                                                                                                                                                                                              19-JUL-2000; 2000WO-US19774.
                                                                                                                                                                                                                                                                                                                                                                      29-MAR-2001
                                                                                                                                                                                                                                                                                                  (EPIM-) EPIMMUNE INC
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                     145 SPGQRV 150
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1 spgqrv 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPGQRV 150
                                                                                                                                                                                                                   composition useful as a vaccines against hepatitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Conserv
                                           h 2.1%; Score 6; DB Similarity 100.0%; Pred. No. 4. 6; Conservative 0; Mismatches
                                                                                                                                                                                                                                                               Sidney J,
Celis E,
                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                   AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ŗ,
                                                                                                                                                                                                                                                                                                                          99US-0357737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.1%;
100.0%;
                                                                                                                                                                                                                                                               Southwood S, Livi
Kubo RT, Grey HM;
                                                                                                                                                                                            214pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                   vaccine;
                                                                                                                                                                                                                                                                           Livingston BD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . No.
                                                       DB 22; Le
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB
. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   immunogen; HLA-binding
                                                                Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 9;
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                                             Indels
                                                                                                                                                                                                                                                                            Chesnut
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                                                                                                                                                                                                                                                                            77
                                                                                                                                                                                                                     virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in humans. The
                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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                                            Gaps
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                                            0;
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RESULT 1
Qy
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                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                             Hepatitis C virus;
                                                                                                                                Hepatitis C
                                                                                                                                                  02-JUL-2001
                                                                                                                                                                   AAJ03766;
                                                                                                                                                                                     AAJ03766 standard;
                                                                                                                                                                                                                                                                                                                                     The present invention describes a composition comprising a prepared hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121. These are derived from HCV HIA-binding motifs. They are useful in vaccines for the prevention and treatment of HCV infection in humans. The present sequence is an epitope used in the disclosure of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                              A new composition useful as a vaccines against hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-308046/32.
          19-JUL-1999;
                            19-JUL-2000; 2000WO-US19774
                                              29-MAR-2001
                                                                WO200121189-A1
                                                                                  Hepatitis C
                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                             Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antiviral.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hepatitis C virus epitope #2605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAJ02614;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAJ02614 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-JUL-2000; 2000WO-US19774.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200121189-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hepatitis C virus; HCV; epitope; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (EPIM-) EPIMMUNE INC
                                                                                                                                                                                                                                                    145 SPGQRV 150
                                                                                                                                                                                                       13
                                                                                                                                                                                                                                  2 spgqrv 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sidney J,
Celis E,
                                                                                                                                                                                                                                                                                                                      9
                                                                                                                               virus epitope #3757.
                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                           Page 164; 214pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                     ΑĄ,
                                                                                                                                                (first entry)
          99US-0357737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0357737.
                                                                                                             HCV;
                                                                                                                                                                                     Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide; 9
                                                                                                                                                                                                                                                                                2.1%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Southwood S, Livi
Kubo RT, Grey HM;
                                                                                                             epitope;
                                                                                                                                                                                     9 AA
                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                Score 6;
Pred. No.
                                                                                                                                                                                                                                                                        Mismatches
                                                                                                             vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Livingston BD,
                                                                                                                                                                                                                                                                                DB 22; L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immunogen; HLA-binding motif;
                                                                                                             immunogen;
                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chesnut
                                                                                                             HLA-binding
                                                                                                                                                                                                                                                                                         9;
                                                                                                                                                                                                                                                                                                                                                                                                               virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ₽,
                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                      Gaps
                                                                                                            motif;
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XXCCCCCX PX PX XX
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AAJ03901
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PI
PI
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PR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 6
                                                                                                                                                             Sette A,
Baker DM,
                    The present invention describes a composition comprising a prepared hepatitis C virus (HCV) epicope such as those given in AAJ0010-AAJ04121. These are derived from HCV HLA-binding motifs. They are useful in vaccines for the prevention and treatment of HCV infection in humans. The present sequence is an epitope used in the disclosure of the invention.
                                                                                                                                                                       Sette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   145 SPGQRV 150
||||||
1 spgqrv 6
                                                                                                                A new composition useful as a vaccines against hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes a composition comprising a prepared hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121. These are derived from HCV HLA-binding motifs. They are useful in vaccines for the prevention and treatment of HCV infection in humans. The present sequence is an epitope used in the disclosure of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sette
Baker
                                                                                           Example
                                                                                                                                        WPI; 2001-308046/32
                                                                                                                                                                                                                       19-JUL-1999;
                                                                                                                                                                                                                                                                                            WO200121189-A1
                                                                                                                                                                                                                                                                                                                                          Hepatitis C antiviral.
                                                                                                                                                                                                                                                                                                                                                                           Hepatitis C virus epitope #3892.
                                                                                                                                                                                                                                                                                                                                                                                                  02-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                        AAJ03901;
                                                                                                                                                                                                                                                                                                                                                                                                                                               AAJ03901 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A new composition useful as a vaccines against hepatitis C virus
Sequence
                                                                                                                                                                                               (EPIM-) EPIMMUNE INC
                                                                                                                                                                                                                                              19-JUL-2000; 2000WO-US19774
                                                                                                                                                                                                                                                                     29-MAR-2001.
                                                                                                                                                                                                                                                                                                                  Hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 185; 214pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-308046/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (EPIM-) EPIMMUNE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14
                                                                                         2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 6; Conserv
                                                                                                                                                            Sidney J,
Celis E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sidney J,
Celis E,
                                                                                         Page 193; 214pp;
9
                                                                                                                                                                                                                                                                                                                                                    virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
AA;
                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                       99US-0357737
                                                                                                                                                                                                                                                                                                                                                     HCV;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide; 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.1%;
100.0%;
                                                                                                                                                             Southwood Kubo RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Southwood S, Livingston Kubo RT, Grey HM;
                                                                                                                                                                                                                                                                                                                                                    epitope;
                                                                                         English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 6;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         English
                                                                                                                                                                                                                                                                                                                                                                                                                                               A
                                                                                                                                                             S, Livingston Grey HM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                    vaccine; immunogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 22; NO. 4.3e+05; 0;
                                                                                                                                                                          BD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
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                                                                                                                                                                                                                                                                                                                                                    HLA-binding
                                                                                                                                                                          R;
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                                                                                                                virus
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Query Match

2.1%;

Score

6

DB 22;

Length

9;

Best Local Similarity 100.0%; Pred. No. 4.3e+05; Matches 6; Conservative 0; Mismatches 0;

Indels

0; Gaps

0

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AAY49753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q
                                                                                                                                                                                                            A composition (A) comprises at least a first dimerisation peptide (I) C comprising the sequence (SI) that is no more than 8 amino acids long, where the composition optionally comprises a second dimerisation peptide (C (II): NH2-X1-X2-X3-X4-X5-COOH (SI) where X1 to X4 = Ala, Val, Ile, Leu, Trp, Phe, Met, or Tyr, and X5 = Lys, Arg, Asp or Glu; CC NH2-X1-X2-X3-X4-X5-COOH (II). The compositions of the invention are cidsplayed intracellularly or extracellularly and are useful to identity comprises and molecules, and to modulate intracellular signalling C pathways. A library of constrained proteins may be evaluated in vivo for its bloactive potential. The invention can be used to access molecules cor targets within living cells, and then provide for the isolation of the constrained protein which has a phenotypic effect on the living cells. The methods are also useful to identify in vitro binding partners CC of the constrained protein. The compositions of the invention are useful CC as a scaffold for gene therapy and for potential use as a therapeutic negative constrained protein. The propositions of the invention are useful CC in physiological fluids. The present sequence is used in the
                                                        Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes peptides which have a moderate or high affinity for each other, when added as extensions to both the N-terminus and C-terminus of a protein, can be used to help fold the protein into a compact structure. This compact structure is more stable to proteases.
                                                                                                                                                            Sequence
                                                                                                                                                                                                in physiological fluids. The present sequence exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 18; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel dimerization peptides which self-associate are used with other proteins to effect the formation of compact structures -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-620191/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anderson D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Compact structure forming peptide; dimerisation; stability; scaffold; library screening; drug screening; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Compact structure forming exemplification peptide #46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY49753;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY49753 standard; peptide; 10 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (RIGE-) RIGEL PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-OCT-1999.
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241 VQRKRQ 246
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                                                                                                                                                            10
                                                          2.1%; Score 6; DB:
ilarity 100.0%; Pred. No. 79
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                            AΑ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98US-0080444
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                                                                                 DB 20;
o. 79;
                                                            0;
                                                                                                 Length 10;
                                                              Indels
                                                            0;
                                                            Gaps
                                                            0;
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Db 3 vqrkrq 8

Search completed: January 24, 2002, 16:25:45 Job time: 130 sec

Title: Perfect score:

US-08-741-095B-26 283

OM protein - protein search, using sw model

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January 24,

2002, 16:23:35

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Scoring table:

Maximum

DB

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length:

30

Database :

Issued_Patents_AA:*

Post-processing: Listing first 45

summaries

Total number of hits satisfying

chosen

parameters:

Word size Searched:

0

212252 seqs, Gapop 60.0 , OLIGO

22503292 residues

Gapext 60

429, App
9, App)1
670, App
4, App)1
503, App
4, App)1
60, App)1
60, App)1
10, App)1
119, App)1
110, App)1

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is the number of results predicted by chance to have a ater than or equal to the score of the result being printed, rived by analysis of the total score distribution.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/backfiles1.pep:*
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Patent No. 5204326
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Sequence 2, Appli
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Sequence 9, Appli
Sequence 1, Appli
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APPLICANT: Haaf, Thomas

APPLICANT: Ilya Golub, Efim

APPLICANT: Reddy, Gurucharan

APPLICANT: Reddy, Gurucharan

APPLICANT: Radding, Charles M.

APPLICANT: Ward, David C.

TITLE OF INVENTION. WETHODS AND COMPOSITIONS UTI

FILE REFERENCE: A-65680/RFT/RMS

CURRENT APPLICATION NUMBER: US/09/007,020

CURRENT FILING DATE: 1998-01-14

EARLIER APPLICATION NUMBER: 60/035,834

EARLIER FILING DATE: 1997-01-30

EARLIER APPLICATION NUMBER: 60/045,668

EARLIER FILING DATE: 1997-01-30
                                                                                                          RESULT 2
US-08-789-333F-9
; Sequence 9, Application US/08789333F
; Patent No. 6153380
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US-09-007-020-3
GENERAL INFORMATION:
APPLICANT: NO. 6153380an, Garry P
APPLICANT: Rothenberg, S. M.
TITLE OF INVENTION: METHODS FOR SCREENING
TITLE OF INVENTION: EFFECTOR PEPTIDES AND
FILE REFERENCE: A642601DJBRMSDSS
CURRENT APPLICATION NUMBER: US/08/789,333F
CURRENT FILLING DATE: 1997-01-23
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Best Local S
Matches 6
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NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 10
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Patent No. 6090539
                                                                                                                                                                                                                                                                                                                               FEATURE:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Artificial Sequence
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US-09-042-107-429
PCT-US94-01840-9
US-08-444-818-670
US-09-139-802-4
US-07-942-245-503
US-08-363-691-6
US-08-363-691-6
US-08-340-283-184
US-08-464-250-19
US-08-464-250-19
PCT-US95-02121-149
US-08-212-190-10
US-08-212-190-10
US-08-212-190-10
US-08-310-10
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SUMMARIES

US-09-007-020-3 US-08-789-333F-9 US-09-169-015-19 US-09-133-944-9

5204326-83 5204326-84

US-07-818-781A-1 US-07-817-916A-1 US-08-003-839-1 PCT-US93-06278-1

Gaps

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PCT-US95-13841-2 5204326-86 5204326-87 5204326-90

US-08-59-5 US-08-928-958-5 US-08-928-958-5 US-09-072-429-5 US-08-392-816-9 US-08-132-164-1 US-08-098-1123-164-1 US-09-173-941-16

is derived

No.

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TITLE OF INVENTION: Green Fluorescent Protein Fusions with Random Peptides; FILE REFERENCE: A6690/DJB/RWS/SJR
CURRENT APPLICATION UMBER: US/09/169,015; CURRENT FILING DATE: 1998-10-08; NUMBER OF SEQ ID NOS: 55
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 19
LENGTH. 10
                                                                                                                                                 US-09-133-944-9
; Sequence 9, Application US/09133944
; Patent No. 6280937
; GENERAL INFORMATION:
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APPLICANT: Luo, Ying
APPLICANT: Yu, Pei Wen
APPLICANT: Lorens, James
APPLICANT: Lorens, James
TITLE OF INVENTION: SHUTTLE VECTORS
FILE REFERENCE: A66252/DJB/DAV
CURRENT APPLICATION NUMBER: US/09/133,944
CURRENT FILING DATE: 1999-08-14
EARLIER APPLICATION NUMBER: 09/133,949
EARLIER FILING DATE: 1998-08-14
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SEQ ID NO 9
LENGTH: 10
TYPE: PRT
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Matches 6; Conserv
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PRIOR FILING DATE: 1996-01-23
NUMBER OF SEQ ID NOS: 102
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PAGES: 961-
DATE: 1990
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TYPE: PRT
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100.0%; Pred. No. 26;
tive 0; Mismatches
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100.0%; Pred. No. 26;
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RESULT 6
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;APPLICANT: FUJII, SETSURO;YANAMOTO, YOSHIHITO;SHIMIZU, FUMIO
;INAI, MASATOSHI;KINOSHITA, NAOSUMI;NAKAMURA, SHIZUO;HIROHASHI,
;MITSURU; SAKAMOTO, TAKASHI;TSUTSUMI, KAZUHIKO;SHIRASAKA, TETSUHIKO
;TITLE OF INVENTION: POLYPEPTIDE DERIVATIVES AND CALCIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 5
5204326-81
;Patent No. 5204326
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NUMBER OF SEQUENCES: 147
CURRENT APPLICATION DATA:
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                                                                                                                             SEQ ID NO:82:
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Matches 6; Conserv
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SOFTWARE: PatentIn Ver. SEQ ID NO 9
                   Query Match
Best Local (
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JOURNAL: Cell
VOLUME: 62
PAGES: 1019-1019
DATE: 1990
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                                                                                                                                                                                CURRENT APPLICATION DATA:
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                                                                                                                                           FILING DATE: 14-MAR-1990
                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                            15 TPRTDV 20
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2.1%; Score 6; DB (
100.0%; Pred. No. 30;
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                                      DB 6;
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RESULT 8
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Best Local :
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                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Chang, Tse Wen
TITLE OF INVENTION: Making antibodies to antigenic epitopes present on B cell but
TITLE OF INVENTION: surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: AMINO ACID
TOPOLOGY: line
818-70--
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APPLICATION NUMBER: 07/
FILING DATE: 11/16/1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PS/2
OPERATING SYSTEM: DOS 3.30
SOSTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: DNA encoding antibodies to antigenic epitopes present on TITLE OF INVENTION: basophil surface
                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                     NUMBER OF SEQUENCES:
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COUNTRY: US
                                                                                                                                                                                                                                                                                                                                       247 EAEGEA 252
                                    CITY: Houston
STATE: Texas
                                                                                                                                                                                                                                                                                                                                                                    Local Similarity nes 6; Conserv
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REGISTRATION NUMBER: 31.
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: UP ZIP: 77025
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STATE: Texas
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                                                                 STREET:
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                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                        8 EAEGEA 13
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                                                                   E: Tanox Biosystems, Inc
10301 Stella Link Rd.
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(713) 664-8914
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                                                                                                                                                                                                                                                                                                                                                                      Conservative
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100.0%; Pred. No. 34
ative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application Patent No. 5292867 GENERAL INFORMATION:
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CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/27
APPLICATION NUMBER: 11/16/1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (713) 664-89
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                       OPERATING SYSTEM: DOS 3.30
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
COMPUTER: IBM PS/2
                                                                                                                                                           CLASSIFICATION: 530 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Mirabel, Eric P.
REGISTION NUMBER: 31,211
REFERENCE/DOCKET NUMBER: TN
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION: TELEPHONE: (713) 664-2288
                                                                         APPLICATION NUMBER: 07/817,918
FILING DATE: 1/6/9
APPLICATION NUMBER: 07/272,243
FILING DATE: 11/16/198
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Peptides representing antigenic epitopes present on B cell TITLE OF INVENTION: surface
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SOFTWARE: Wordper
                                              NAME: Mirabel, Eric P. REGISTRATION NUMBER: 3
                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                        OPERATING SYSTEM:
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ZIP: 77025
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nes 6; Conserv
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                              REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                               APPLICATION NUMBER: US/08/003,839
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10301 Stella Link Rd.
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100.0%; Pred. No.
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                                            31,211
                                TNX88-03BBB
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RESULT 11
5204326-83
;Patent No. 5204326
; APPLICANT: FUJII, SETSURO;YAMAMOTO, YOSHIHITO;SHIMIZU, FUMIO;INAI, MASATOSHI;KINOSHITA, NAOSUMI;NAKAMURA, SHIZUO;HIROHASHI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-003-839-1
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APPLICATION NUMBER: 07/468,766

APPLICATION NUMBER: 01/23/1990

ATTORNEY/AGENT INFORMATION:

NAME: Mirabel, Eric P.

REGISTRATION NUMBER: 31,211

REFERENCE/DOCKET NUMBER: TIN88-0

TELEPHONE: (713) 664-2288

TELEPHONE: (713) 664-8914

INFORMATION FOR SED ID NO: 1:
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Best Local Similarity
Matches 6; Conserv
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Best Local Similarity
Matches 6; Conserv
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Chang, Tse Wen
TITLE OF INVENTION: PEPTIDES REPRESENTING ANTIGENIC EPITOPES OF
TITLE OF INVENTION: PRESENT ON B CELL BUT NOT BASOPHIL SURFACE
                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PS/2
OPERATING SYSTEM: DOS 3.30
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Diskette, 3.5 inch
                                                                                                                                                        247 EAEGEA 252
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ZIP: 77025
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CITY: Houston
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                                                                                                                         8 EAEGEA 13
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                                                                                                                                                                                                                                                                                                                            14 amino acids
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Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                  linear
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100.0%; Pred. No. 34;
tive 0; Mismatches
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o. 34;
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Best Local Similarity
Thes 6; Conserve
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; Patent No. 5204326
; Patent No. 5204326
; Patent No. 5204326
; APPLICANT: FUJII, SETSURO; YAMAMOTO, YOSHIHITO; SHIMIZU, FUMIO; INAI, MASATOSHI; KINOSHITA, NAOSUMI; NAKAMURA, SHIZUO; HIROHASHI, SHITSURU; SAKAMOTO, TAKASHI; TSUTSUMI, KAZUHIKO; SHIRASAKA, TETSUHIKO; TITLE OF INVENTION: POLYPEPTIDE DERIVATIVES AND CALCIUM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5204326-83
                                                                                                                                                                                            FILING DATE: 14-MAR-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;METABOLISM IMPROVING AGENT
; NUMBER OF SEQUENCES: 147
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/493,359
; FILING DATE: 14-MAR-1990
; SEQ ID NO:84:
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;Patent No. 5204326
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; NUMBER OF SEQUENCES: 147
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                                                                                                                                                                                                                                                                     METABOLISM IMPROVING AGENT NUMBER OF SEQUENCES: 1
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APPLICATION NUMBER: US/07/493,359
FILING DATE: 14-MAR-1990
SEQ ID NO:83:
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Best Local Similarity
Matches 6; Conser
                                                                      Matches
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Best Local Similarity
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                                 15 TPRTDV 20
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4 TPRTDV 9
5 TPRTDV 10
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                                                                   2.1%; Score 6; DB 6;
100.0%; Pred. No. 36;
tive 0; Mismatches
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100.0%; Pred. No.
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0; Mismatches
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В
; MOLECULE TYPE:
PCT-US95-13841-2
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: United Biomedical Inc; Walfield, Alan M.;
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: Synthetic IgE Membrane Anchor
TITLE OF INVENTION: Poptide Immunogens for the Treatment of Allergy
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: MATIA C. H. Lin
STREET: 345 Park Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 6; Conserv
                                                   TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
                                                                                                                               APPLICATION NUMBER: 08/328,519
FILING DATE: 25-OCT-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Lin, Maria C.H.
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4117
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: 25-OCCCLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: US
ZIP: 10154
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: New York
STATE: NY
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                             TOPOLOGY:
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                             amino acid
)GY: linear
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           peptide
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Query Match

2.1%;

Score 6;

DB 5;

Length 17;

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Best Local Similarity 100.0%; pred. No. 40;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 247 EBEGEA 252

Db 9 EABGEA 14
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Search completed: January 24, 2002, 16:26:05 Job time: 150 sec

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Result
No.
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Maximum DB
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                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                 Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq length:
seq length:
        66775
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/cgn2_6/ptodata/2/paa/US092_COMB.pep:*
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 PCT-US99-20180-51
7 US-09-342-767-51
PCT-US99-20180-50
17 US-09-342-767-50
17 US-09-342-767-50
18 US-09-086-582-21
18 US-09-724-059-21780
19 US-09-724-059-34140
19 US-09-357-737-1617
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820.990 Million cell updates/sec
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Sequence 51, Appl
Sequence 50, Appl
Sequence 50, Appl
Sequence 50, Appl
Sequence 21, Appl
Sequence 21780, A
Sequence 34140, A
Sequence 1066, Ap
Sequence 1617, Ap
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	equence 1, App	equence 252	equence 1734,	e 1673,	e 1378,	e 1067	equence 203,	277,	664	3387	e 2529	e 173	e 1673	e 1378	e 1067	e 203, Āp	e 77, Ap	3664,	e 3387,	e 2	e 1734,	equence 1673,	equence 137	e 1067,	equence 203,	equence 7	e 82,	e 82,	e 95	101,	90	82, App	e 1617,	1066	1617,	σ,	

ALIGNMENTS

QΥ SOFTWARE: FastSEQ for Windows Version 3.0; SEQ ID NO 51; LENGTH: 25; TYPE: PRT ORGANISM: Homo sapiens
PCT-US99-20180-51 멍 PCT-US99-20180-51 Query Match Best Local Similarity Matches 25; Conserv Sequence 51, Application PC/TUS9920180
GENERAL INFORMATION:
APPLICANT: Millennium Biotherapeutics, Inc.
TITLE OF INVENTION: NOVEL MOLECULES OF THE H
TITLE OF INVENTION: PROTEIN FAMILY AND USES
FILE REFERENCE: 09404/079WO1 CURRENT APPLICATION NUMBER: PCT/US99/20180
CURRENT FILING DATE: 1999-09-03
EARLIER APPLICATION NUMBER: US 09/342,767
EARLIER FILING DATE: 1999-06-29
EARLIER APPLICATION NUMBER: US 09/146,950
EARLIER APPLICATION NUMBER: US 09/146,950
EARLIER FILING DATE: 1998-09-03
UNMBER: OF SEQ ID NOS: 58 201 WVWWFLSGSLVIVIVCSTVGLIICV 225 1 WVWWFLSGSLVIVIVCSTVGLIICV 25 Conservative 8.8%; Score 25; Pred. No. 0; Mismatches Inc.
THE HERPESVIRUS-ENTRY-MEDIATOR-RELATED DB 1; 9.9e-17 THEREOF Length 25 Indels 0, 0

US-09-342-767-51

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-342-767-51
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Sequence 50, Application US/09342767
GENERAL INFORMATION:
APPLICANT: Busfield, Samantha J.
APPLICANT: Busfield, Samantha J.
TITLE OF INVENTION: NOVEL MOLECULES OF THE
TITLE OF INVENTION: HERPESVIRUS-ENTRY-MEDIATOR-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
FILE REFERENCE: MBT098-061CP1
CURRENT APPLICATION NUMBER: US/09/342,767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 50
LENGTH: 22
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Millennium Biotherapeutics, Inc.
TITLE OF INVENTION: NOVEL MOLECULES OF THE HERDESVIRUS-ENTRY-MEDIATOR-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
FILE REFERENCE: 09404/079901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 25; Conserv
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 51
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                      Query Match 7.8%;
Best Local Similarity 100.0%;
Matches 22; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 50,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: PCT/US99/20180 CURRENT FILING DATE: 1999-09-03 EARLIER APPLICATION NUMBER: US 09/342,767 EARLIER FILING DATE: 1999-06-29 EARLIER APPLICATION NUMBER: US 09/146,950 EARLIER FILING DATE: 1998-09-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/342,767
CURRENT FILING DATE: 1999-06-29
EARLIER APPLICATION NUMBER: US 09/146,950
EARLIER FILING DATE: 1998-09-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Busfield, Samantha J.
TITLE OF INVENTION: NOVEL MOLECULES OF THE
TITLE OF INVENTION: HERPESVIRUS-ENTRY-MEDIATOR-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: MBIO98-061CP1
                                                                                                                                                                                                                                                                                                           165 CPPGTFSPNGTLEECQHQTKCS 186
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100.0%; Pred. No.
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; Pred. No.
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8.6e-14;
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9.9e-17;
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RESULT

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; MOLECULE TYPE:
US-09-086-582-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Homo sapiens US-09-342-767-50
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LENGTH: 22
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 21, Application US/09086582 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                          Matches
                                                                                    Query Match
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EARLIER APPLICATION NUMBER: US 09/146,950
EARLIER FILING DATE: 1998-09-03
NUMBER OF SEQ ID NOS: 58
SOFTWARE: PastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                  TELEFAX: (301) 309-84:
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: KENLEY K. HOOVER
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PF36
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIDIM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA
APPLICATION NUMBER: US/09/086,582
                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 15 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: NI, JIAN APPLICANT: MOORE, PAUL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: HUMAN TUMOR NECROSIS FACTOR TITLE OF INVENTION: RECEPTOR-LIKE PROTEIN 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                             263 DYTTVAVEETIPSFT 277
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                                                         Local Similarity
nes 15; Conserv
                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                       FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
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9410 KEY WEST AVENUE
                                                                                                                                                                                                                                                     (301) 309-8439
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                                                          Conservative
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100.0%; Pred. No.
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Pred. No.
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                                                         Mismatches
                                                                        DB 14;
. 5.7e-07;
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US-09-724-059-21780

GENERAL INFORMATION

Application US/09724059

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Query Match
Best Local Similarity
7; Conserve
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Best Local Similarity
---hos 7; Conserva
                                                                                            US-09-357-737-1066
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                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Polypeptide sequence US-09-724-059-34140
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                                                                                                               RESULT
                                                               Sequence 1066, Application US/09357737 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: GB9710809.6
PRIOR FILING DATE: 1997-05-23
NUMBER OF SEQ ID NOS: 1407122
SOFTWARE: MacAllLister
SEQ ID NO 21780
LENGTH: 25
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: MacAllLister
SEQ ID NO 34140
LENGTH: 25
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TITLE OF INVENTION: Nucleic Acid Binding Proteins
FILE REFERENCE: P2500USM
CURRENT APPLICATION NUMBER: US/09/724,059
CURRENT FILING DATE: 2000-11-28
                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: GB9710809.6 PRIOR FILING DATE: 1997-05-23 NUMBER OF SEQ ID NOS: 1407122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/724,059
CURRENT FILING DATE: 2000-11-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Isalan, Mark
TITLE OF INVENTION: Nucleic Acid Binding Proteins
FILE REFERENCE: P2500USM
                                                 APPLICANT:
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APPLICANT: Klug, Aai
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APPLICANT: Klug, Aaron
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                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
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14 RTDVLRL 20
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                                                 Sette, Alessandro
Sidney, John
Southwood, Scott
Livingston, Brian
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100.0%; Pred. No.
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5.86;
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Best Local Similarity
Watches 6; Conserva
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PRIOR FILING DATE: 1998-11-10
PRIOR PAPLICATION NUMBER: U.S. S.N. 08/205,713
PRIOR FILING DATE: 1994-03-04
PRIOR APPLICATION NUMBER: U.S. S.N. 08/159,184
PRIOR FILING DATE: 1993-11-29
PRIOR PRIOR APPLICATION NUMBER: U.S. S.N. 08/073,205
PRIOR FILING DATE: 1993-06-04
PRIOR APPLICATION NUMBER: U.S. S.N. 08/027,146
PRIOR APPLICATION NUMBER: U.S. S.N. 08/027,146
PRIOR FILING DATE: 1993-03-05
                                                                                           SOFTWARE: Fas:
SEQ ID NO 1617
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SEQ ID NO 1066
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ORGANISM: Hepatitis C Virus -09-357-737-1617
                                                                                                                  PRIOR APPLICATION NUMBER: U.S.S.N. 08/027,
PRIOR FILING DATE: 1993-03-05
NUMBER OF SEQ ID NOS: 3681
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: U.S.S.N. 09/189,702
PRIOR FILING DATE: 1998-11-10
PRIOR APPLICATION NUMBER: U.S.S.N. 08/205,713
PRIOR FILING DATE: 1994-03-04
PRIOR APPLICATION NUMBER: U.S.S.N. 08/159,184
PRIOR PRIOR PRIOR DATE: 1993-11-29
PRIOR PRIOR APPLICATION NUMBER: U.S.S.N. 08/073,205
PRIOR FILING DATE: 1993-16-04
PRIOR FILING DATE: 1993-06-04
PRIOR FILING DATE: 1993-06-04
                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/357,737 CURRENT FILING DATE: 1999-07-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: INDUCING CELLULAR RESPONSES TO HEPATITIS TITLE OF INVENTION: C VIRUS USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS FILE REFERENCE: 18623-014000US
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TYPE: PRT
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CURRENT FILING DATE: 1999-07-19
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TITLE OF INVENTION: C VIRUS USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
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Best Local Similarity
"hes 6; Conserve
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                                                                                                                                                                                                                                                                                  RESULT
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PRIOR FILING DATE: 1998-11-10
PRIOR APPLICATION NUMBER: U.S.S.N. 08/205,713
PRIOR FILING DATE: 1994-03-04
PRIOR APPLICATION NUMBER: U.S.S.N. 08/159,184
PRIOR APPLICATION NUMBER: U.S.S.N. 08/073,205
PRIOR APPLICATION NUMBER: U.S.S.N. 08/073,205
PRIOR APPLICATION NUMBER: U.S.S.N. 08/073,205
PRIOR APPLICATION NUMBER: U.S.S.N. 08/027,146
PRIOR APPLICATION NUMBER: U.S.S.N. 08/027,146
PRIOR FILING DATE: 1993-03-05
PRIOR FILING DATE: 1993-03-05
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Best Local Similarity
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                                                                                                                                                                                                                                              Sequence 1617, Application US/09357737A
                                                                                          APPLICANT:
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TITLE OF INVENTION: C VIRUS USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
FILE REFERENCE: 18623-014000US
CURRENT APPLICATION NUMBER: US/09/357,737A
CURRENT FILING DATE: 1999-07-19
                 TITLE OF INVENTION: INDUCING CELLULAR RESPONSES TO HEPATITIS
TITLE OF INVENTION: C VIRUS USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
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                                                       APPLICANT:
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                                                                                        Baker,Denise
Celis,Esteban
                                                                                                                              Chesnut, Robert
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Celis,Esteban
                                                   Grey, Howard
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                                                                                                                                                                 Southwood, Scott
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                                                                       Kubo, Ralph
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18623-014000US
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100.0%; Pred. No.
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Query Match
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                                                                                                                                                                              ; SOFTWARE: Fast
; SEQ ID NO 1066
; LENGTH: 8
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PRIOR FILING DATE: 1998-11-10
PRIOR APPLICATION NUMBER: U.S.S.N. 08/205,713
PRIOR FILING DATE: 1994-03-04
PRIOR APPLICATION NUMBER: U.S.S.N. 08/159,184
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: U.S.S.N. 08/073,205
PRIOR FILING DATE: 1993-06-04
PRIOR APPLICATION NUMBER: U.S.S.N. 08/027,146
PRIOR APPLICATION NUMBER: U.S.S.N. 08/027,146
PRIOR APPLICATION NUMBER: U.S.S.N. 08/027,146
PRIOR FILING DATE: 1993-03-05
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LENGTH: 8
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/357,737B CURRENT FILING DATE: 1999-07-19 PRIOR APPLICATION NUMBER: US 08/027,146 PRIOR FILING DATE: 1993-03-05 PRIOR APPLICATION NUMBER: US 08/073,205 PRIOR APPLICATION NUMBER: US 08/159,184 PRIOR APPLICATION NUMBER: US 08/159,184
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APPLICANT:
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PRIOR APPLICATION NUMBER: US 08/205,713
PRIOR FILING DATE: 1994-03-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Inducing Cellular Responses to Hepatitis C
TITLE OF INVENTION: Virus Using Peptide and Nucleic Acid Compositions
FILE REFERENCE: 018623-014000US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/357,737A CURRENT FILING DATE: 1999-07-19
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                                                                                                                                          ORGANISM: Hepatitis
                                                                                                                                                                TYPE:
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Best Local Similarity
"hehes 6; Conserva
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; OTHER INFORMATION: HIV NS5 2615, peptide 1292.23
PCT-US00-23913-82
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PRIOR FILING DATE: 1993-03-05
PRIOR APPLICATION NUMBER: US 08/073,205
PRIOR FILING DATE: 1993-06-04
PRIOR PPLICATION NUMBER: US 08/159,184
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/205,713
PRIOR FILING DATE: 1994-03-04
PRIOR FILING DATE: 1994-03-04
PRIOR APPLICATION NUMBER: US 09/189,702
PRIOR APPLICATION NUMBER: US 09/189,702
PRIOR FILING DATE: 1998-11-10
                                                  SOFTWARE: FASTSEQ FOR WINDOWS
SEQ ID NO 82
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                           Sequence 82, Application PC/TUS0023913 GENERAL INFORMATION:
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                                                                                                                                     APPLICANT: Epimmune Inc.
TITLE OF INVENTION: HLA Binding Peptides and Their Uses
FILE REFERENCE: 18623-80-5PC
CURRENT APPLICATION NUMBER: PCT/US00/23913
CURRENT FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 127
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Epimmune Inc.
TITLE OF INVENTION: Inducing Cellular Responses to Hepatitis C
TITLE OF INVENTION: Virus Using Peptide and Nucleic Acid Compositions
FILE REFERENCE: 018623-014000US
CURRENT APPLICATION NUMBER: US/09/357,737B
CURRENT FILING DATE: 199-07-19
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SOFTWARE: FastSEQ for Windows Version 4.0
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                                      FEATURE:
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No. 2.9e+06;
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Search completed: January 24, 2002, 16:28:09 Job time: 184 sec

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Sequence 90, Application:
Sequence 90, Application:
GENERAL INFORMATION:
APPLICANT: SETTE, Alessandro
APPLICANT: SIDNEY, John
TITLE OF INVENTION: HLA BINDING PEPTIDES AND THEIR USES
TITLE OF SEQUENCES: 288
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                                                            Query Match
Best Local Similarity
Matches 6; Conser
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Best Local Similarity
Matches 6; Conserv
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FILING DATE: 21-JUL-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
                                                                                                                                                                                                                                                          TELEFAX: 415/543-5043
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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ADDRESSEE: Townsend and Townsend Khourie and Crew.
STREET: One Market Plaza, Steuart Street Tower, 20th
                                                                                                                                                             MOLECULE TYPE:
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                              145 SPGQRV 150
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SYSTEM: PC-DOS/MS-DOS
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100.0%; Pred. No. 2.
tive 0; Mismatches
                                                                            2.1%; Score 6;
100.0%; Pred. No
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                                                              Mismatches
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Maximum DB
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Perfect score:
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     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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       /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep:*
/cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*
/cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*
/cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*
/cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*
/cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep:*
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US-09-916-940-9
US-09-572-404B-1338
US-08-816-011E-16
US-08-816-011E-16
US-08-816-011E-18
US-08-816-011E-18
US-08-816-011E-18
US-08-816-011E-18
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US-09-881-636-38
US-09-881-636-38
US-09-881-636-39
US-09-881-636-39
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US-09-881-636-104
US-09-881-636-109
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US-09-881-636-109
US-09-881-636-701
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US-09-572-404B-727
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Similarity 6; Conser 6; Conser KRQ 246	CATION N G DATE: CATION N G DATE: CATION N G DATE: CATION N EQ ID NO atentin N artifici	1 29, Application in 19, Application in 19, Application in 19, Application of INVENTION: GETIVENTION: GETIVENTION: GETIVENTION: GETIVENTION THE APPLICATION NUMB FILING DATE: APPLICATION NUMB FILING DATE: APPLICATION NUMB FILING DATE: CONTROL NUMB FILIN	
2.1%; 100.0%; tive ion US/0	UMBER: US 08/5 1996-01-23 1996-01-23 1996-01-23 1997-01-23 UMBER: US 08/7 1997-01-23 S: 102 Ver: 2.0 Ver: 2.0	tion US/0991694(: : : : : : : : : : : : : : : : : : :	110 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5
Score 6: DB 5: L Pred. No. 22; 0; Mismatches 0 9572404B	,7589,911 ,789,933 ,787,738 ,787,738 of Artificia n sequence.	ALIGNMENTS 1940 SCREENING FOR EPTIDES AND RNAMS 709/916,940 7727,715	US-09-572-404B-158 US-09-572-404B-377 US-09-572-404B-377 US-09-513-333-54 US-09-522-900-52 US-09-539-382-52 US-09-20-954-11 US-10-100-568-31 US-10-1010-568-31 US-09-974-879-318 US-09-974-879-318 US-09-402-17-284 US-09-766-253-164 US-09-766-253-164 US-09-766-253-164 US-09-766-253-164 US-09-766-253-164 US-09-766-253-164 US-09-766-253-164 US-09-766-253-164 US-09-766-253-164 US-09-766-253-164
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US-08-816-011E-10
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TITLE OF INVENTION: PARASSIUM CHANNELS, NUCLEOTIDE SEQUENCES
FILE REFERENCE: 01142.0122 SEQUENCE LISTING
CURRENT APPLICATION NUMBER: US/08/816,011E
CURRENT FILING DATE: 1997-03-11
PRIOR APPLICATION NUMBER: 08/332,312
PRIOR FILING DATE: 1994-10-31
PRIOR FILING DATE: 1995-10-25
NUMBER OF SEQ ID NOS: 67
SOFTWARE: PATENTIN VET: 2.1
SEQ ID NO 10
LENGTH: 24
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GENERAL INFORMATION:
APPLICANT: Pausch, Mark H
APPLICANT: Price, Laura A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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                                                                                                    APPLICANT: PAUSCH, MARK H
APPLICANT: PTICE, LAURA A
APPLICANT: PTICE, LAURA A
TITLE OF INVENTION: POTASSIUM CHANNELS, NUCLEOTIDE SEQUENCES ENCODING THEM,
TITLE OF INVENTION: AND METHODS OF USING SAME
TILE REFERENCE: 01142.0122 SEQUENCE LISTING
CURRENT APPLICATION NUMBER: US/08/816,011E
CURRENT FILING DATE: 1997-03-11
PRIOR APPLICATION NUMBER: 08/332,312
PRIOR FILING DATE: 1994-10-31
PRIOR APPLICATION NUMBER: PCT/US95/14364
PRIOR FILING DATE: 1995-10-25
NUMBER OF SEQ ID NOS: 67
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tive 0; Mismatches
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Query Match
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; ORGANISM: Drosophila melanogaster US-08-816-011F-18
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US-08-816-011F-10
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                                                    SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 18
LENGTH: 24
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GENERAL INFORMATION:
APPLICANT: Pausch, Mark H
APPLICANT: Price, Laura A
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PRIOR FILING DATE: 1995-10-25
NUMBER OF SEQ ID NOS: 67
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 10
LENCTH: 24
TYPE: PRT
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Matches 6; Conserv
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                                                                                                                                    TITLE OF INVENTION: POTASSIUM CHANNELS, NUCLEOTIDE SEQUENCES ENCODING THEM, TITLE OF INVENTION: AND METHODS OF USING SAME FILE REFERENCE: 01142.0122 SEQUENCE LISTING CURRENT APPLICATION NUMBER: US/08/816,011F CURRENT FILING DATE: 1997-03-11 PRIOR APPLICATION NUMBER: 08/332,312 PRIOR APPLICATION NUMBER: 08/332,312 PRIOR FILING DATE: 1994-10-31 PRIOR FILING DATE: 1994-10-31 PRIOR FILING DATE: 1995-10-25
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                                                                                                                   NUMBER OF SEQ ID NOS: 67
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; ORGANISM: Homo sapiens US-09-881-636-38
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; LOCATION: (1)...(7)
; OTHER INFORMATION: synthetic construct
PCT-US01-28124A-17
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Sequence 17, Application PC/TUS0128124A
GENERAL INFORMATION:
APPLICANT: Board of Regents, The University of Texas System
FITLE OF INVENTION: Biopanning and Rapid Anaylsis of Selective Interactive Ligands;
FILE REFERENCE: 005774, P004PCT
CURRENT APPLICATION UNBER: PCT/US01/28124A
CURRENT FILING DATE: 2001-09-07
NUMBER OF SEQ ID NOS: 289
          Query Match
Best Local Similarity 100.0%; Pred. No. 1...
Matches 5; Conservative 0; Mismatches
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CURRENT FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: 60/211,454
                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: 55P414: GENE EXPRESSED IN VARIOUS TITLE OF INVENTION: CANCERS FILE REFERENCE: 129.12USU1
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                                                                                                                                                        LENGTH: 9
TYPE: PRT
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NUMBER OF SEQ ID NOS: 720
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ORGANISM: Artificial Sequence
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3 LSGSL 7
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Steve Chappell Mitchell
Arthur B. Raitano
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100.0%; Pred. No. 46;
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                                                                                                                                     ; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 128
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-881-636-128
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APPLICANT: Steve Chappell Mitchell
APPLICANT: Arthur B. Raitano
APPLICANT: Aya Jakobovits
TITLE OF INVENTION: 55P4H4: GENE EXPRESSED
TITLE OF INVENTION: CANCERS
FILE REFERENCE: 129.12USU1
CURRENT FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: 60/211,454
PRIOR APPLICATION NUMBER: 60/211,454
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                                                Best Local Similarity
Matches 5; Conserv
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Best Local Similarity
Matches 5; Conserv
                                                                                  Query Match
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TITLE OF INVENTION: 55P4H4: GENE EXPRESSI
TITLE OF INVENTION: CANCERS
FILE REFERENCE: 129.12USU1
CURRENT APPLICATION NUMBER: US/09/881,636
CURRENT FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: 60/211,454
PRIOR FILING DATE: 2000-06-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Mary Faris
APPLICANT: Rene S. H
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Daniel E.H. Afar
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Steve Chappell Mitchell
Arthur B. Raitano
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Daniel E.H. Afar
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 339
                                                              Matches
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Best Local :
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SEQ ID NO 236
LENGTH: 9
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CURRENT FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: 60/211,454
PRIOR FILING DATE: 2000-06-13
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CURRENT FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: 60/211,454
PRIOR FILING DATE: 2000-06-13
NUMBER OF SEQ ID NOS: 720
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TITLE OF INVENTION: 55P4H4: GENE EXPRESSED IN VARIOUS
TITLE OF INVENTION: CANCERS
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nes 5; Conserv
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Daniel E.H. Afar
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Daniel E.H. Afar
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; SOFTWARE: FASTSEQ FOR WII
; SEQ ID NO 532
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-881-636-532
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Best Local Similarity
Thes 5; Conserv
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                                                                              Query Match
Best Local :
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SEQ ID NO 426
LENGTH: 9
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CURRENT FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: 60/211,454
PRIOR FILING DATE: 2000-06-13
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TITLE OF INVENTION: 55P4H4: GENE EXPRESSI
TITLE OF INVENTION: CANCERS
FILE REFERENCE: 129.12USU1
CURRENT APPLICATION NUMBER: US/09/881,636
CURRENT FILING DATE: 2001-06-13
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APPLICANT: Rene S. H
APPLICANT: Daniel E.
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TITLE OF INVENTION: CANCERS
FILE REFERENCE: 129.12USU1
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APPLICANT: Rene S. Hubert
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Steve Chappell Mitchell
Arthur B. Raitano
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Daniel E.H. Afar
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US-09-881-636-633

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Sequence 633, Application US/09881636

Sequence 633, Application US/09881636

Sequence 633, Application US/09881636

Sequence 633, Application US/09881636

GENERAL INFORMATION:

APPLICANT: Baniel E.H. Afar

APPLICANT: Baniel E.H. Afar

APPLICANT: Athor B. Ratiano

APPLICANT: Athor B. Ratiano

APPLICANT: Athor B. Ratiano

APPLICANT: Athor B. Ratiano

INFORMATION: SAPAHH: GENE EXPRESSED IN VARIOUS

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pilin, type IV - /
                                                                                                                      phosphoprotein pho melittin - giant h
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pilin type Ae1 -
                                                                                   hypothetical prote tropomyosin 1, bra
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ALIGNMENTS	B44817 PT0629 PT0512 PT0728 S08995 A49823 A44960 A43976 B43976 B43976 S11545 S11545 S11545 A05166 A05174 A93147 A93147	
	34.5K structural p 35K structural pro T-cell receptor be T-cell receptor be T-cell receptor be pyertrehalosemic adipokinetic hormo neuropeptide Led-C hypertrehalosemic hypertrehalosemic adipokinetic hormo neuropeptide M-I oxytocin - hippopo oxytocin - spotted oxytocin - finback oxytocin - Austral	

R; Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991
A; Title: Junctional sequences of fetal T
A; Reference number: PT0509; MUID:91277601
A; Accession: PT0715
A; Accession: PT0715

T cell receptor beta chains have few N regions

C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0715

RESULT 1
PT0715
T-cell receptor beta chain V-D-J region (165-3A) - mouse (fragment)

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RESULT 2
B43590
pilin type Ae6 - Aeromonas hydrophila (fragment)
C; Species: Aeromonas hydrophila
C; Species: 12-Jan-1993 #sequence_revision 12-Jan-1993 #text_change 17-Nov-2000
                                         Query Match
Best Local Similarity
Thes 5; Conserve
                                                                                                                                                                               R;Hokama, A.; Iwanaga, M.
Infect. Immun. 59, 3478-3483, 1991
A;Title: Purification and characterization of Aeromonas sobria pili, a possible colon A;Reference number: A43590; MUID:91372953
A;Accession: B43590
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                                                                                                                       A; Molecule type: protein A; Residues: 1-10 <HOK> C; Superfamily: Vibrio che
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Best Local Similarity
"~+~hes 5; Conserv
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A;Molecule type: DNA
A;Residues: 1-6 <PEE>
A;Experimental source: newborn thymus, strain BALB/c
C;Keywords: T-cell'receptor
 Вþ
                                                                                                                                                                A; Status: preliminary
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6 LVIVI 10
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Pred. No.
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No. 2.2e+02;
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C:Accession: PC4055
R:Harriott; O.T.; Hosted, T.J
Gene 161, 63-67, 1995
A;Title: Sequences of nifX, n
A; Reference number: JC4203; M
A; Accession: PC4055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: protein
A; Residues: 1-10 < RAM>
R; Kamo, M.; Kawakami, T.; Ts
submitted to JIPID, March 19
A; Reference number: PA0109
A; Accession: PA0107
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Best Local Similarity
""" onservi
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A; Accession: A43590
A:Status
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C:Species: Aeromonas sobria
C:Date: 12-Jan-1993 #sequence_revision 12-Jan-1993 #text_change 18-Jun-1993
               A; Molecule type: DNA
A; Residues: 1-13 <HAR>
                                                                                                                                   hypothetical 13 protein - Frankia sp. (fragment) C;Species: Frankia sp. C;Date: 10-Sep-1995 #sequence_revision 27-Oct-19 C;Accession: PC4055
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein QA100052 - Arabidopsis thaliana (fragment)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 06-Jun-1997
C;Accession: PA0050; PA0107
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Best Local Similarity
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Infect. Immun. 59, 3478-3483, 1991
A; Title: Purification and characte
A;Cross-references: GB:L29299
                                                                                                                                                                                                                                                                                                                                                                                                                            A; Experimental source: root
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A; Accession: PA0050
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6 LVIVI 10
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1995
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3. 2.2e+02;
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pilin - Aeromonas sobria (fragment)
C;Species: Aeromonas sobria
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 17-Nov-2000
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A;Reference number: PH0746; MUID:92078846
A;Accession: PH0773
A;Reference number: A47678; MUID:93018994 A;Contents: TAP13
                                         A; Title: Characterization of Aeromonas sobria TAP13 pili: a possible new colonization
                                                        J. Gen. Microbiol. 138, 1913-1919, 1992
                                                                            R; Iwanaga, M.; Hokama,
                                                                                                 C; Accession: A47678
                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
When 5; Conservi
                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Keywords: T-cell receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: mRNA
A;Residues: 1-16 <CAS2
A;Cross-references: EMBL:X60868; NID:g50247; PIDN:CAA43257.1;
A;Experimental source: T lymphocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   K;Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Accession: PH0773
R; Casanova, J.L.; R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T-cell receptor beta chain (C7) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Nov-1999
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Watches 5; Conserv.
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A;Molecule type: protein
A;Residues: 1-15 <CHA>
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R;Chaudhuri, S.; Duncan, K.; Graham, L.D.; Coggins, J.R.
Biochem. J. 275, 1-6, 1991
A;Title: Identification of the active-site lysine residues of two biosynthetic 3-dehy A;Reference number: S14749; MUID:91207275
A;Accession: S14749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3-dehydroquinase - Neurospora crassa (fragment)
C;Species: Neurospora crassa
C;Date: 21-Nov-1993 #sequence_revision 01-Sep-1995 #text_change 01-Sep-1995
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Best Local Similarity
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5. 3.1e+02
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5. 2.7e+02;
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A;Accession: A47678
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-17 <IWA>
A;Note: sequence extracted from NCBI backbone (NCBIP:116639)
C;Superfamily: Vibrio cholerae prepilin-like 17.3K protein type
photosystem I 14.1K E3 chain
C; Species: Nicotiana tabacum
                                 PQ0687
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                                                                                                                                                                                                                                                     C; Keywords: chloroplast;
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A;Title: Molecular heterogeneity of photosystem I. psaD, psaE, p. A;Reference number: PQ0667; MUID:94105345
                                                                                                                                                                                                                                                                                                                                                                                         C; Accession:
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                                                                                                                                                                                                                                                                                                                                                                                                                         photosystem I 14.0K E4 chain - common tobacco (fragment)
C; Species: Nicotiana tabacum (common tobacco)
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Best Local Similarity
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A;Description: Conservation of a methylation imprint and a putative imprinting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 05-Nov-1999
C;Accession: S58277
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                                                  RESULT 11
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A; Accession: PQ0688
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A; Accession: S58277
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Keywords: growth factor
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                                                                                                                                                                                                                                                       photosynthesis;
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Pred. No.
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               (fragment)
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3.6e+02;
es 0; Indels
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C;Genetics:
                                                    A;Status: preliminary;
A;Molecule type: DNA
A;Residues: 1-21 <RES>
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Best Local Similarity
Thehes 5; Conserve
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A; Residues: 1-21 <RES>
A; Cross-references: GB: M34478; NID:g143851; PIDN:AAA98049.1; PID:g143852
C; Superfamily: tetracycline resistance protein
C; Keywords: antibiotic resistance; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Obokata, J.; Mikami, K.; Hayashida, N.; Nakamura, Plant Physiol. 102, 1259-1267, 1993 A;Title: Molecular heterogeneity of photosystem I. | A;Reference number: PQ0667; MUID:94105345 A;Accession: PQ0687
                                                                                                                   A; Areference number: 158423; MUID: 95218835
                                                                                                                                                              R; Mimura, J.; Ema, M.; Sogawa, K. Pharmacogenetics 4, 349-354, 1994
                                                                                                                                                                                                                 C;Species: Mus sp. (mouse)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Reference number: I40157; MUID: 90253151
A; Accession: I40157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tetracycline resistance (tet) protein - plasmid pBC16 (fragment) C;Species: plasmid pBC16
C;Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change
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C;Accession: PQ0687; PQ0675
                                     A; Cross-references:
                                                                                                             A; Accession: I58423
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A; Residues: -1-20
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Best Local
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Title: Expression of Bacillus thuringiensis
                                                                                                                                                                                                                                                                                                                                                                                 186 SWLVT 190
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                                   GB:S76844; NID:g913085; PIDN:AAB33978.1; PID:g913086
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                                                                                          translated
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Pred. No.
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R;Kreil, G.

R;Kreil, G.

R;Kreil, G.

R;Ritle: The structure of Apis dorsata melittin: phylogenetic relationships between hone A;Reference number: A01763; MUID:75168194

A;Recession: A01763

A;Accession: A01763

A;Molecule type: protein
A;Mesidues: 1-26 (KRE)
C;Superfamily: melittin major
C;Superfamily: melittin major
C;Keywords: amidated carboxyl end; homotetramer
F;26/Modified site: amidated carboxyl end (Glu) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:Z77735; PIDN:CAB01294.1
C;Superfamily: phosphoprotein phosphatase; phosphoesterase core homology; phosphoprotein
C;Keywords: phosphoric monoester hydrolase
Search completed: January 24, 2002, 16:26:28 Job time: 113 sec
                                                                                                                   В
                                                                                                                                                             δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      melittin - giant honeybee (tentative sequence)
C;Species: Apis mellifera dorsata (giant honeybee)
C;Date: 22-Jun-1981 #sequence_revision 22-Jun-1981 #text_change 31-Mar-2000
C;Accession: A01763
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A; A; Accession: T42257
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A;Molecule type: DNA
A;Residues: 1-24 <ZEK>
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                                                                                                                                                                                                            Query Match 1.8%; Score 5; DB 1; Len Best Local Similarity 100.0%; Pred. No. 5e+02; Matches 5; Conservative 0; Mismatches 0;
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Best Local Similarity
Matches 5; Conserv
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Best Local Similarity
Matches 5; Conserv
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|||||
4 DVLRL 8
                                                                                                                                                                     243 RKRQE 247
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13 KRRKP 17
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100.0%; Pred. No. 4.7e+02;
1.ve 0; Mismatches 0;
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Perfect score:
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OXYT_SQUAC
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ESL_LACCA
COXH_ONCMY
ESL_LACCA
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5 zea mays (m
3 clostridium
5 salmonella
6 thiobacillu
4 chionoecete
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9 cyprinus ca
8 oryctolagus
0 squalus aca
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1 homo sapien
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	llarity Conserva 18	56 CCCA HE MA 119	NMTE STANDARD; PRT; 1996 (Rel. 34, Created) 1996 (Rel. 37, Last sequence u 1998 (Rel. 37, Last annotation DE DEHYDROGENASE, BETA CHAIN (E tas testosteroni (Pseudomonas t ta; Proteobacteria; beta subdiv xID=285;	1111111111
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P01502;
21-JUL-1986
21-JUL-1986
20-AUG-2001
                                                                                          Hemolysis;
MOD_RES
SEQUENCE
                                                                                                                                                                                                             between honeybees as deduced from sequence data.";
FEBS Lett. 54:100-102(1975)
-i- FENCTION: MAIN TOXIN OF BEE VENOM WITH STRONG HEMOLYTIC ACTIVITY.
INTEGRATES INTO CELL MEMBRANES AND HAS MULTIPLE EFFECTS, PROBABLY AS A RESULT OF ITS INTERACTION WITH NEGATIVELY CHANGED PHOSPHOLIPIDS. IT INHIBITS WELL KNOWN TRANSPORT PUMPS SUCH AS THE NA(+)-K(+)-ATPASE AND THE H(+)-K(+)-ATPASE. INCREASES THE PERMEABILITY OF CELL MEMBRANES TO IONS, PARTICULARLY NA+ AND INDIRECTLY CA2+, BECAUSE OF THE NA(+)-CA(2+)-EXCHANGE.
-i- SUBUNIT: MOMOMER AND HOMOTETRAMER (BY SIMILARITY).
-i- SUBUNIT: MOMOMER AND HOMOTETRAMER (BY SIMILARITY).
-i- DATABASE: NAME-FIOTEIN SPOLLIGHT;
NOTE-ISSUE 12 Of July 2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Apis dorsata (Giant honeybee).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Ac
Apoidea; Apidae; Apis.
NCBI_TaxID=7462;
                                                                                                                                                 Pfam; PF01372; Melittin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS50240; TRYPSIN_DOM; PARTIAL. PROSITE; PS00134; TRYPSIN_HIS; PARTIAL. PROSITE; PS00135; TRYPSIN_SER; PARTIAL.
                                                                                                                                     ProDom;
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HSSP; P01501; 2MLT.
                                                                                                                                                              InterPro;
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nes 5; Conserv
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PTM: EXTENSIVELY GLYCOSYLATED.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN
TRYPSIN FAMILY.
; S38295; S38295.
; P23946; IKIT.
pps: CA1 317
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                                                                                                                                                                                                    WWW="http://www.expasy.org/spotlight/articles/sptlt012.html"
                                                                                                                                    PD014636;
                                                                                                                                                              IPR002116; Melittin.
                                                                                                          Toxin;
26
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26 AMIDA
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01, Last sequence update)
40, Last annotation update)
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RESULT 4

EOSI_HUMAN STANDARD;

ID EOSI_HUMAN STANDARD;

AC p02731;

DT 21-JUL-1986 (Rel. 01, Last sell)

DT 21-JUL-1986 (Rel. 01, Last sell)

TO 21-JUL-1986 (Rel. 01, Last sell)

DT 21-JUL-1986 (Rel. 01, Last sell)

EOSINOPHILOTACTIC PEPTIDES.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata;

OC Mammalia; Eutheria; Primates;

OX NCBI_TAXID=9606;

RN [1]

RP SEQUENCE.

RX MEDLINE-76078412; PubMed=1066;

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DT 01-FEB-1991 (Rel. 1:
DT SEX PHEROMONE CPD1.
OS Enterococcus faecal:
OC Enterococus faecal:
OC Enterococus faecal:
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RA SUZULT FANIONI
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                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-85040388; PubMed-6436978; Suzuki A., Mori M., Sagakami Y., Craig R.A., Clewell D.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 72:4123-4127(1975).

-i- MISCELLANEOUS: THESE PEPTIDES ARE RELEASED FROM MAST CELLS IN (AND OTHER TISSUES) DURING HYPERSENSITIVITY REACTIONS (ANAPHYLAXIS). THEIR ACTIVITIES, PREFERENTIALLY AFFECTING EOSINOPHILS, INCLUDE CHEMOTAXIS, CHEMOTACTIC DEACTIVATION, REJORD OF ENZYMES, AND STIMULATION OF THE HEXOSE MONOPHOSPHATE SHUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=76078412; PubMed=1060093;
Goetzl E.J., Austen K.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Purification and synthesis of eosinophilotactic tetrapeptides of human lung tissue: identification as eosinophil chemotactic facto
                                                                                                                                                                                                                                                                                                                                                                         "Isolation and structure of bacterial sex pheromone,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49 VGSE 52
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                                                                                                                                                                                                                                                            BACTERIOCIN PLASMID
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   Conservative (
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13, Last sequence up
17, Last annotation
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100.0%
1.4%; Score 4; DB
100.0%; Pred. No. 1e-
ive 0; Mismatches
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                                                                                                                                                                                        MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Streptococcus faecalis).
Bacillus/Clostridium group; Enterococcaceae;
                                                                                                                                                                                                                                                                   PPD1
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                                                                                                                                                                                        8665B729C682C729 CRC64
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/FTId=VAR_005201.
6B05B862A0000000 CRC64;
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0; Mismatches
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0. le+05;
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                                                                                                                                                                                                                                PIR; A05169; A05169.
PIR; S08995; S08995.
PIR; A49823; A49823.
PIR; A44960; A44960.
                                    Neuropeptide;
MOD_RES
MOD_RES
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01-FEB-1994 (Rel. 28, Last annotation update)
HYPERTREHALOSAEMIC FACTOR I (NEUROPEPTIDE M.I) (PERIPLAN
(PEA-CAH-I) (LED-CC-I) (HYPERTREHALOSAEMIC NEUROPEPTIDE
Periplaneta americana (American cockroach),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaede G., Rinehart K.L. Jr.;

"Primary structures of hypertrehalosaemic neuropeptides isolated from the corpora cardiaca of the cockroaches Leucophaea maderae,

Gromphadorhina portentosa, Blattella germanica and Blatta orientalis and of the stick insect Extatosoma tiaratum assigned by tandem fast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Blatta orientalis (Oriental cockroach).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
Blattoidea; Blattidae; Periplaneta.
NCBI_TaxID-6978, 7539, 6976;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPECIES=B.orientalis; TISSUE=Corpora cardiaca; MEDLINE=90253659; PubMed=2340112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPECIES-B.orientalis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The metabolic neuropeptides of the corpus cardiacum beetle and the American cockroach are identical.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-90160053;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPECIES=L.decemlineata;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Isolation and primary structure of two peptides with cardioacceleratory and hyperglycemic activity from the cardiaca of Periplaneta americana."; proc. Natl. Acad. Sci. U.S.A. 81:5575-5579(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=84298179; PubMed=6591205; Scarborough R.M., Jamieson G.C., Miller C.A., Schooley D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=84298179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPECIES=P.americana;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Structures of two cockroach neuropeptides assigned bombardment mass spectrometry."; biochem. Biophys. Res. Commun. 124:350-358(1984).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P04548;
13-AUG-1987
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Witten J.L., Schaffer M.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-85046530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HTF1_PERAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Leptinotarsa decemlineata (Colorado potato beetle),
                                                                                                                                                                                                                                                                                                                                                                    m bombardment mass spectrometry.";

1. Chem. Hoppe-Seyler 371:345-354(1990),

1. Chem. Hoppe-Seyler 371:345-354(1990),

1. Chem. Hoppe-Seyler 371:345-354(1990),

1. Chem. Hoppe-Seyler 371:355-354(1990),

1. Chem. Hoppe-Seyler 371:355-354(19
                                                                                                                                                                PS00256; AKH; 1.
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                                                                                                                    Amidation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         neata; TISSUE=Corpora
PubMed=2576128;
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ffer M.H., O'Shea
        991 MW;
PYRROLIDONE CARBOXYLIC ACID.
AMIDATION.
86745775B9C452D6 CRC64;
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Best Local S
Matches 4
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Best Local
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P23879;
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P25419;
01-MAY-1992
                                                        Cyprinus carpio (Common carp), and Petromyzon marinus (Sea lamprey). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes; Cyprinidae; Cyprininae; Cyprinus.
                                                                                                                            01-NOV-1991 (Rel.
01-NOV-1991 (Rel.
01-NOV-1995 (Rel.
                                                                                                                                                                                                                                                                                                                                                MOD_RES
SEQUENCE
SPECIES=C.carpio;
Acher R., Chauvet
"Characterization
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01-FEB-1994 (Rel.
01-FEB-1994 (Rel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-1992 (Rel. 22, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
HYPERTREHALOSAEMIC FACTOR (HOTH) (HYPERTREHALOSEMIC NEUROPEPTIDE).
                                     SEQUENCE.
                                                                                                                      VASOTOCIN.
                                                                                                                                                                                                                                                                                                                                                                      Neuropeptide;
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The primary structure of the hypertrehalosemic neuropeptide tenebrionid beetles: a novel member of the AKH/RPCH family."; Peptides 11:455-459(190).
-i- FUNCTION: HYPERTREHALOSAEMIC FACTORS ARE NEUROPEPTIDES TH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaede G., Rosinski
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=90341081; PubMed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tenebrio molitor (Yellow mealworm), and Zophobas rugipes.
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B43976;
                                                                                                                                                                                                                                                                                                                                                                                                                                  THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH (TREHALOSE THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).

SIMILARITY: BELONGS TO THE AKH / HRTH / BDOWN THE A43976; A43976
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PS00256; AKH; 1.
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                                                                                                                                                                              STANDARD;
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TISSUE=Pituitary;
J., Chauvet M.-T., Crepy D.;
of neurohypophyseal hormones
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32,
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1005
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Last annotation update)
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86745775B9C44736 CRC64;
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Pred. No.
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Pred. No.
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  fresh water bony
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Best Local Similarity
Matches 4; Conserv
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P32878; P01188;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence up
15-DEC-1998 (Rel. 37, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                              LT 9
_RABIT
                                                                                                                                                                                                              MEDLINE-72215060; PubMed-5150741; Chauvet J., Chauvet M.-T., Acher R.; "Evolution of neurohypophyseal hormones: principles from rabbits and rats.";
                                                                                                                                                                                                                                                                                                   Oryctolagus cuniculus (Rabbit), Hippopotamus amphibius (Hippopotamus), Balaenoptera physalus (Finback Whale) (Common rorqual), Tachyglossus aculeatus aculeatus (Australian echidna), and Hydrolagus colliei (Spotted ratfish) (Pacific ratfish). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Lagomorpha; Leporidae; Oryctolagus. NCBI_TaxID=9986, 9833, 9770, 49271, 7873;
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MOD_RES
SEQUENCE
SPECIES-A.aculeatus;
               SEQUENCE
                                                          SPECIES-B.physalus;
Acher R., Chauvet J
                                                                                                                    "Arginine and lysine vasopressins in the hippopotamus neurohypophysis.";
                                                                                                                                                                                                                                                                    SPECIES-Rabbit;
                                                                                                                                                                                                                                                                                                                                                                                       OXYTOCIN (OCYTOCIN).
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                                    Nature
                                                                                                                                                       MEDLINE=71232719;
                                                                                                                                                                     SPECIES-H.amphibius;
                                                                                                                                                                                                        Biochimie
                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPECIES=P.marinus; TISSUE=Pituitary; MEDLINE=88225976; PubMed=3371648; Lane T.F., Sower S.A., Kawauchi H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                             Ferguson D.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Petromyzon marinus): isolation and amin
Gen. Comp. Endocrinol. 70:152-157(1988).
-i- FUNCTION: ANTIDIURETIC HORMONE.
                                               "Isolation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00220; hormone4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Arginine vasotocin from the pituitary gland of the lamprey petromyzon marinus): isolation and amino acid sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE;
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                                                                                  EQUENCE.
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SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY
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S06375; S06375.
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                                    201:191-192(1964).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PS00264; NEUROHYPOPHYS_HORM;
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                                           Chauvet J., Chauvet M.-T
                                                                                                                                                                                                        53:1099-1104(1971).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        carp (Cyprinus carpio). Comparison with hormones
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                                                                                                          Endocrinol.
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                                                                                                                                            Pickering
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1053
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                                                                                                         13:425-429(1969)
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                                                                                                                                            B.T.;
                                              oxytocin
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17EB176EB456D04B CRC64;
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Pred. No.
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                                              vasopressin.";
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RESULT
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Best Local Similarity
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OXYY_SQUAC
P43000;
01-NOV-1995
01-NOV-1995
01-NOV-1995
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PIR; A91466; A91466.
PIR; A92774; A92774.
PIR; A93147; A93147.
PIR; A93408; A93408.
PIR; B90667; B90667.
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          PROSITE;
Hormone;
                                                     MEDIINE-72128038; pubMed=4622083;
Acher R., Chauvet J., Chauvet M.-T., Fontaine M.;
Spiny dog-fish (Squalus acanthias)."
C. R. Acad. Sci., D. Sci. Nat. 274:313-316(1972).
-I- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
                                                                                                                                                           MEDIJUE-73031727; PubMed-5083097; Acher R., Chauvet J., Chauvet M.-T.; Phylogeny of the neurohypophysial lisolated from a cartilaginous fish, Eur. J. Biochem. 29:12-19(1972).
                                                                                                                                                                                                                                                  Squalus acanthias (Spiny dogfish).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Elasmobranchii; Squalea; Squaloidei; Squalidae; Squalus.
NCBI_TaxID=7797;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Oxytocin as a neurophyophysial hormone elasmobranch fish, Hydrolagus collei."; J. Endocrinol. 45:597-606(1969).
                                 Pfam; PF00220;
                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                    VALITOCIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=73223515; PubMed=4515919; Acher R., Chauvet J., Chauvet M.-T. "Neurohypophysial hormones and evol
                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  163 QNCP 166
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                    D0220; hormone4; 1.
PS00264; NEUROHYPOPHYS_HORM; 1.
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PS00264; NEUROHYPOPHYS_HORM;
          Amidation.
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                                          IPR000981; Neurhypophys_horm.
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32, Last sequences
32, Last annotations
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annotation
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17F8376EB456D04B CRC64;
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                                                                                                                                                                           hormones. Two new active peptides Squalus acanthias.";
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1e+05;
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Best Local :
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                                                                                                                                                                                  ESL_LACCA STANDAKU;
ESL_LACCA STANDAKU;
P81758;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
30-MAY-2000 (Rel. 39, East annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
01-OCT-1994 (Rel. 30, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation update)
CYTOCHROME C OXIDASE POLYPEPTIDE VIC (EC 1.9.3.1) (FRAGMENT).
Oncorllynchus myklss (Rainbow trout) (Salmo gairdneri).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleoste
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ONCMY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lopez de Felipe F.;
Submitted (MAR-1999) to the
                                                            STRAIN-IFPL731;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 FERRICYTOCHROME C.
-!- SUBCELLULAR LOCATION: MITOCHONDRIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus NCBI_TaxID-8022;
                                                                                   SEQUENCE
                                                                                                                      NCBI_TaxID=1582;
                                                                                                                                                                 Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                           101 PAMG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=94237150; PubMed=8181469;
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                                                                                                                                                            Bacillus/Clostridium group;
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01-FEB-1995 (Rel. 31, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
GENERAL STRESS PROTEIN 9 (GSP9) (FRAGMENT).
the cockroach
isoforms.";
                                                      Muren J.E., Naessel D.R.;
"Isolation of five tachykinin-related
                                                                                                                    TISSUE=Midgut;
MEDLINE=97053012; PubMed=8897641;
                                                                                                                                                                                                                                                                        Pterygota; Neoptera; Orth
Blaberoidea; Blaberidae;
                                                                                                                                                                                                                                                                                                                                     Leucophaea maderae (Madeira cockroach).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Microbiology 140:741-752(1994).
-!- INDUCTION: BY HEAT SHOCK, SALT STRESS,
LIMITATION AND OXYGEN LIMITATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Voelker U., Engelmann S., Maul
Schmid R., Mach H., Hecker M.;
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Bacillus/Staphylococcus
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Regul. Pept. 65:185-196(1996). [2]

isoforms.

Peptides 18:7-15(1997)

"Seven tachykinin-related peptides isolated from the brain of madeira cockroach; evidence for tissue-specific expression of

the

Muren J.E., Naessel D.R.; MEDLINE=97269266; PubMed=9114447;

TISSUE-Brain;

SEQUENCE, AND MASS SPECTROMETRY.

-:- FUNCTION: MYOACTIVE PEPTIDE. INCREASES THE AMPLITUDE AND FREQUENCY
OF SPONTANEOUS CONTRACTIONS AND TONUS OF HINDGUT MUSCLE.
-:- TISSUE SPECIFICITY: MIDGUT AND BRAIN.
-:- MASS SPECTROMETRY: MW=1033.2; METHOD=MALDI.
-:- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
Tachykinin; Neuropeptide; Amidation.
MOD_RES
10
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AMIDATION.
SEQUENCE 10 AA; 1033 MW; C452CD66D9C8769n CPC64.

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LPW_THETH
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P05624;
01-NOV-1988
01-NOV-1988
30-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN+HB8 / ATCC 27634;
MEDLINE-89000781; Pubmed-2844259;
MEDLINE-89000781; Pubmed-284259;
Sato S., Nakada Y., Kanaya S., Tanaka T.;
"Molecular cloning and nucleotide sequence of Thermus thermophilus
"Molecular cloning and nucleotide sequence of Thermus thermophilus
"HB8 trpE and trpG.";
Biochim. Biophys. Acta 950:303-312(1988).
-i- FUNCTION: THIS PROTEIN IS INVOLVED IN CONTROL OF THE BIOSYNTHESIS
                                                                                                                                                   EMBL; X07744; CAA30565.1; -.
PIR; S03315; LFTWWE.
Tryptophan biosynthesis; Leader peptide.
SEQUENCE 11 AA; 1228 MW; 364B295A772DC5A7 CRC64;
                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
TRP OPERON LEADER PEPTIDE.
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||||
2 PAMG 5
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Bacteria; Thermus/Deinococcus group; Thermus group; Thermus.
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ALPS 5
                                                                   Conservative
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Search completed: January 24, 2002, 16:29:16 Job time: 191 sec

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Q9q2n4 chlamydosau	Q9g350 laudakia sa				Q9g5v6 phrynocepha	Q9g5v9 laudakia st			Q9g5x4 trapelus ag		9	Q9g673 ctenophorus	079985 laudakia ca		079921 phrynocepha	Q16217 homo sapien		8 moloney m	Q99213 aegilops sq	P82384 drosophila	Q9tlm7 laurencia v	Q9tuy0 monodelphis	Q9yiq9 human adeno	Q9yir0 human adeno	Q9yve3 human adeno

ALIGNMENTS

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O9FUX5
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O1-MAR-2001 (TrEMBLrel. 16, Created)
O1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
O1-MAR-2001 (TrEMBLrel. 16, Last annotation update)
MAXY (FRAGMENT).
Symphoricarpos albus.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=91372953; PubMed=1680105; Hokama A., Iwanaga M.; "Purification and characterization of Aeromonas sobresible colonization factor."; Infect. Immun. 59:3478-3483(1991). SEQUENCE 10 AA; 1143 MW; 4C19F942C72B1057 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Aeromonas sobria.
Bacteria; Proteobacteria; gamma subdivision; Aeromonadaceae;
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5; Conserv
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nilarity 100.0%;
Conservative 0
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Deshpande R.G., Khan M.B., Bhat D.A., Navalkar R.G.,
"Immunoaffinity chromatographic isolation of a high;
seroreactive protein from Mycobacterium leprae cell;
FEMS Immunol. Med. Microbiol. 11:163-169(1995).
SEQUENCE 16 AA; 1842 MW; 54A9ECCA5044F83E CRC64;
 SEQUENCE
                  "Characterization of Aeromonas sobria TAP13 pili: a colonization factor.";
                                                                                                                         01-MAY-2000 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
01-JUN-2000 (TrEMBLrel.
                                                                                                                                                                 Q9R5G4
                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium leprae.
Mycobacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; MCBI_TaxID=1769;
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01-MAY-2000 (TrEMBLrel.
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MLP SUBUNIT (FRAGMENT).
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"Phylogeny and biogeography of T
Harv. Pap. Bot. 5:157-166(2000).
EMBL; AF277633; AAG31453.1; -
NON_TER 1
                                               MEDLINE=93018994; PubMed=1357078
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                                                                                                       Aeromonas
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                                     Iwanaga M., Hokama
                                                                                               Bacteria;
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NCBI_TaxID=13702;
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60A8BF885E6B236C CRC64;
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P82671;
01-OCT-2000
                                                                                                                                                                                                                                                                                                                                         "Purification and characterization of possible new colonization factor."; Microb. Pathog. 13:325-334(1992). SEQUENCE 20 AA; 2171 MW; 38BE2BH
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01-OCT-2000 (TrEMBLrel. 15, Last sequence of the control of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=93225795; PubMed=1363704;
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TION: CHLOROPLAST
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                                                                                                                                                                                    DB 2; I
). le+03;
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8.8e+02;
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   Q52266;
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Q9T2I9;
01-MAY-2000
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09T218;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
14.1 KDA PHOTOSYSTEM I PSAE PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=94105345; PubMed=8278548; Obokata J., Mikami K., Hayashida N., Nakamura Obokata J., Mikami K., Hayashida N., Nakamura "Molecular heterogeneity of photosystem I. psc "Molecular heterogeneity of portions in Nicotiana psat are all present in isoforms in Nicotiana Plant Physiol. 102:1259-1267(1993).

SEQUENCE 20 AA; 1822 MW; E458944E2F5E5D94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chloroplast
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SEQUENCE 20 AA; 1822 MW; A894589439282E5D CRC6
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01-MAY-2000 (TYEMBLIEL 13, Last sequence update)
01-JUN-2000 (TYEMBLIEL 14, Last annotation update)
14 KDA PHOTOSYSTEM I PSAE PROTEIN (FRAGMENT).
NICOLIANA SYLVESTI'S (Wood tobacco).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=4096;
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b. 1e+03;
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. psaD, psaE, psa
iana spp.";
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Q9R4B4 PRELIMINARY;
Q9R4B4;
01-MAY-2000 (TrEMBLrel. 13,
                                                                                                                                                                                                                                                                                                                                                                                                             Q94374 PRELIMINARY; PRT; 24 AA.
Q94374;
Q1-FEB-1997 (TrEMBLrel. 02, Created)
O1-FEB-1997 (TrEMBLrel. 02, Last sequence update)
O1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                            Zeke T., Gergely P., Dombradi V.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
SIDDEL CATALYTIC ACTIVITY: A PHOSPHOPROTEIN + H(2)O = A PROTEIN ORTHOPHOSPHATE (THIS ENZYME IS SERINE/THREONINE SPECIFIC)
-!- SIMILARITY: TO SERINE/THREONINE SPECIFIC PROTEIN PHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                            EMBL; Z77735; CAB01294.1; -. HSSP; P08129; 1FJM.
                                                                                                                                                                                                                                                                                                                                                                                        Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                    PP1-LIKE SER/THR PROTEIN PHOSPHATASE (FRAGMENT).
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Bacillus thuringiensis
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                                                                                                                                                                                                             Hydrolase; Iron; Manganese.
                                                                                                                                                                                                                        Pfam; PF00149; STphosphatase;
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                      ARYLHYDROCARBON RECEPTOR (FRAGMENT).
Sus scrofa (Pig).
Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
NCBI_TaxID=9823;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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Dmitrenko V.V., Garifulin O.M.,
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Makasone N., Iwanaga M., Yamashiro T., Nakashima K., Albert M.J.;
Makasone N., Iwanaga M., Yamashiro T., Nakashima K., Albert M.J.;
"Aeromonas trota strains, which agglutinate with Vibrio cholerae
Bengal antiserum, possess a serologically distinct fimbrial
colonization factor.";
Colonization factor.";
Microbiology 142:309-313(1996).

SEQUENCE 25 AA; 2697 MW; BFCABF6292A8A533 CRC64;
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Michael N.L., Chang G., d'Arcy L./
                                                                                            Human immunodeficiency virus type 1. Viruses; Retroid viruses; Retroviridae; NCBI_TaxID=11676;
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SEQUENCE 25 AA;
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EMBL; AB034363; BAA93826.1; -.
Interpro; IPR000625; REV.
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Ehrenberg

P.K.,

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RA Busch M.P., Birx D.L., Schwartz D.H.;

RT "Defective accessory genes in a human immunodeficiency virus type 1-

RT infected long-term survivor lacking recoverable virus.";

RL J. Virol. 69:4228-4236(1995).

DR EMBL; U24481; AAA79642.1; --

DR InterPro; IPR000625; REV.

DR Pfam; PF00424; REV; 1.

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SO SEQUENCE 25 AA; 2744 MW; IF922F59A5DF261D CRC64;

Query Match

Best Local Similarity 100.0%; Pred. No. 1.2e+03;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 11:111

Db 15 TVGLI 222

Qy 218 TVGLI 222

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Search completed: January 24, 2002, 16:29:00

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AAW12659	AAW95031	AAY94717	AAW87591	AAW60045	AAY95348	AAY93695	AAY94721	AAY06488	AAW69238	AAW05809	ID
Human herpes simpl	Tumour necrosis fa	Human TR2-receptor	Human tumour necro	Human TNF receptor	Human PRO509 antit	Amino acid sequenc	Human TR2-receptor	Human tumour-assoc	Herpesvirus entry	Human tumour necro	Description

45	44	43	42	41	40	39	38	37	36	35	34	33	32	3	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12
259	259	259	259	259	259	259	259	259	259	260	260	260	260	267.5	267.5	267.5	267.5	267.5	267.5	268.5	276.5	332	377.5	393	393	604.5	604.5	604.5	1058	1060	1068	ω.	1570
16.4		16.4	16.4	•	16.4	16.4	16.4	16.4	•	16.5									•				•	•						•		87.0	99.5
248	235	235	235	235	235	235	227	225	183	461	325	325	207	277	277	277	277	277	276	277	281	278	134	136	136	240	185	185	186	197	193	277	283
21	22	21	21	20	19	19	22	21	16	16	16	13	22	22	22	22	20	14	20	20	21	21	17	21	19	17	21	19	21	21	21	21	20
AAY94718	AAB37685	AAY54443	AAY54441	AAW89234	AAW52270	AAW59665	AAB66981	AAY77463	AAR77421	AAR72504	AAR85071 ·	AAR27865	AAB66980 .	AAB37807	AAB50520	AAB84892	AAY52701	AAR38859	AAY33499	AAY32191	AAY94715	AAY95322	AAW05811	AAY94719	AAW60047	AAW05810	AAY94716	AAW60046	AAY79206	AAY79205	AAY79204	N	AAY05797
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Human type 2 tumou	n 40 k	Wild type N-termna	, Amino acid sequenc	Tumour necrosis in	Tumour necrosis fa	Human soluble tumo	Tnfr2 protein. Un	Primate protein se	BamTP delta53 nerv	p75 Tumour Necrosi	Shope fibroma viru	Rabbit fibroma vir		Human CD40. Homo	Human tumour necro	Human CD40 antigen	Human CD40 protein	₽.	Human CD40 protei	CD40 protein. Uni	Murine CD40 prote	Pig costimulatory	_	TR2-	Human TNF receptor	-	•	Human TNF receptor	Soluble herpesviru		Soluble herpesviru	ne-bou	Herpes virus entry

ALIGNMENTS

RESULT AAW05809 Human; tumour necrosis factor; TNF; receptor; treatment; activation; inhibition; identification; agonist; antagonist; stimulation; T cell; differentiation; mediation; immune; antiviral; response; regulation; growth; protection; HIV; radiation; Chlamydia; infection; immunodeficiency; virus; autoimmune disease; inflammation; septic shock; cerebral; malaria; cachexia; B cell; cancer; graft; host; reaction; rejection; Peptide 31-OCT-1996. Key Human tumour necrosis factor receptor. 30-JUN-1997 AAW05809; AAW05809 standard; Protein; 27-APR-1995; WO9634095-A1. Homo sapiens. detection; antibody; reagent. prevention; apoptosis; cytotoxicity; hybridisation probe; Peptide _ (first entry) 95WO-US05058 /label= sig_peptide 39..283 /label= mat_peptide Location/Qualifiers 283 AA

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AAW69238
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       Homo sapiens
                                                                                                                   Entry mediator gene; herpesvirus; HVEM; tumour necrosis ; gene expression regulator; cellular stress; inflammatory
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW69238 standard; Protein;
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                                                                                    lymphocyte
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                                                                                    regulator; autoimmune response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
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Pred. No. 4.5e-121;
; Mismatches 0;
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                                                                                                                                                     tumour necrosis factor receptor;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                e.g. AP-1 induction, whilst agonistic antibodies may enhance HVEM regulation of such induction. The DNA may be used diagnostically, e.g. to determine if DNA and/or RNA encoding HVEM is present in cells, and to prepare HVEM polypeptide recombinantly. It is also useful to produce non-human transgenic animals (e.g. mice or rats), especially knockout animals containing cells with an altered gene encoding HVEM polypeptide. Such animals are useful in the development and screening of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the invention. The protein is useful in quantitative diagnostic assays for HVEM, in affinity purification of HVEM from recombinant cells/natural sources and in competitive-type receptor binding assays. It can also be used to generate antibodies, also useful in diagnostic assays for HVEM and affinity purification of HVEM. HVEM is believed to be a member of the tumour necrosis factor receptor (TNFR) family, and transient transfection of HVEM into human 293 cells caused marked activation of certain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transcription factors, e.g. AP-1, suggesting that HVEM is involved in regulating gene expression in response to infectious stimuli and cellular stress. The predominant expression of HVEM mRNA in lymphocyte-rich tissues (e.g. spleen and peripheral blood) also suggested it may be a receptor in regulating lymphocyte activity. Antibodies produced may therefore be useful therapeutically, e.g. antagonistic antibodies may be useful to block excessive inflammatory/autoimmune response resulting from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Fig 1; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  e.g. for drug screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Herpesvirus entry mediator polypeptide, HVEM - useful, e.g. in assays for HVEM and to produce antibodies and transgenic anima
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  therapeutically useful reagents.
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                                                     HQTKCSWLYTKAGAGTSSSHWVWWFLSGSLVIVIVCSTVGLIICVKRRKPRGDVVKVIVS
                                                                                                                                                   CSPGHFCIVQDGDHCAACRAYATSSPGQRVQKGGTESQDTLCQNCPPGTFSPNGTLEECQ
VQRKRQEAEGEATVIEALQAPPDVTTVAVEETIPSFTGRSPNH
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                                                                                                                               {\tt cspghfcivqdgdhcaacrayatsspgqrvqkggtesqdtlcqncppgtfspngtleecq}
                                                                                                                                                                                                           yrvkeacgeltgtvcepcppgtyiahlnglskclqcqmcdpamglrasrncsrtenavcg
                                                                                                                                                                                                                                                   YRVKEACGELTGTVCEPCPPGTYIAHLNGLSKCLQCQMCDPAMGLRASRNCSRTENAVCG
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                                                                                                                                                                                                                                                                                                                                                              Score 1578; DB 19;
Pred. No. 4.5e-121;
; Mismatches 0;
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RESULT
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Matches 283
                                                                                                                                                     This sequence represents human PRO509 (UN0329), a protein encoded by the novel cDNA clone DNA50148 (see AAX87264), and a member of the tumour necrosis factor receptor family. Amplification of DNA50148 was observed in various tumour tissues, suggesting a role in tumour formation or growth. Antagonists (e.g. antibodies) directed to PRO509 may have use in cancer therapy. The invention identifies 14 genes (see AAX87254-67) that are amplified in the genome of tumour cells. Such amplification is expected to be associated with overexpression of the gene product and to contribute to tumorigenesis. The encoded proteins (see AAX66477-90) may be useful targets for the diagnosis and/or treatment (including prevention) of certain cancers.
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10-JUN-1998;
10-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-NOV-1998;
05-JAN-1998;
29-APR-1998;
                                                                                                    Sequence
                                                                                                                        and may act as predictors of the prognosis of tumour treatment. Antibodies that bind the proteins are claimed and used in claim cancer diagnostic kits.
                                                                                                                                                                                                                                                                                             Example 1; Fig
                                                                                                                                                                                                                                                                                                                   Antibody against proteins expressed tumor diagnosis and treatment
                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-430385/36
                                                                                                                                                                                                                                                                                                                                                                                      Roy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diagnosis; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human tumour-associated protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY06488 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W09935170-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRO1112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-SEP-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                        (GETH
   ۳,
                       μ.
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sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                       ) GENENTECH INC
                                            100.0%;
al Similarity 100.0%;
283; Conservative 0
                                                                                                                                                                                                                                                                                                                                                      AAX87265
                                                                                                                                                                                                                                                                                                                                                                                       Wood
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UNQ555;
                                                                                                    283 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                 Goddard
                                                                                                                                                                                                                                                                                                                                                                                       ΨI;
                                                                                                                                                                                                                                                                                                                                                                                                                                             98US-0086414.
98US-0088742.
98US-0107783.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98US-0109304.
98US-0070440.
98US-0083500.
                                                                                                                                                                                                                                                                                            24; 162pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99WO-US00106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
201..225
/note= "transmembrane domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       226..283
                                                                                                                                                                                                                                                                                                                                                                                                 A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "cytoplasmic domain"
                                                                                                                                                                                                                                                                                                                                                                                                   Gurney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tumour
                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       283 AA
                                            Score 1578; DB 20;
Pred. No. 4.5e-121;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                 ΑL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              necrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PR0509
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                                                                                                                                                                                                                                                                                                                                                                                                Hillan KJ,
                                                                                                                                                                                                                                                                                                                               neoplastic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              receptor;
                                                                                                                                                                                                                                                                                                                                                                                                 Lawrence
                                             Indels
                                                                                                                                                                                                                                                                                                                               cells,
                                                                 Length
                                                                                                                                                                                                                                                                                                                               useful
                                                                   283;
                                                                                                                                     claimed
                                             0;
                                            Gaps
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RESULT
AAY9471
ID AAY9
XX AAY9
XX AAY9
XX 29-J
XX 29-J
XX Tumc
XX Tumc
KW Chrc
KW Chrc
KW Chrc
KW Inmu
KW Alzh
OX HOMC
XX HOMC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-MAR-1999;
26-MAR-1999;
20-MAY-1999;
06-AUG-1999;
                                                                                                                                                  Nucleic acid molecule encoding a human tumor necrosis factor receptor and its two splice variants, useful for treating arthritis or inflammation, cancer (such as follicular lymphomas) and immunodeficiency disorders -
                                                                                                                                                                                                                                                                                                                                                                                                 (NIJJ/)
(ROSE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chromosome p36.2-p36.3; arthritis; inflammation; autoimmune disease; immunodeficlency; metastasis; haemolytic anaemia; asthma; X-linked SCID; severely combined immunodeficlency; apoptosis inhibition; X-linked SCID; Alzheimer's disease; Parkinson's disease; Crohn's disease.
                                                                                                                                                                                                                                                                   N-PSDB;
                                                                                                                                                                                                                                                                                                                                 Ni J,
                                                                                                           Disclosure;
                                                                                                                                                                                                                                                                                                                                                                             (GENT/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-SEP-2000.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tumour necrosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-JAN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241
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DB; AAA28149.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CSPGHFCIVQDGDHCAACRAYATSSPGQRVQKGGTESQDTLCQNCPPGTFSPNGTLEECQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VQRKRQEAEGEATVIEALQAPPDVTTVAVEETIPSFTGRSPNH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HQTKCSWLYTKAGAGTSSSHWVWWFLSGSLVIVIVCSTVGLIICVKRRKPRGDVVKVIVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TR2-receptor
                                                                                                                                                                                                                                                                                                                                 Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                        NI J.
ROSEN
GENTZ
                                                                                                           Page 370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000WO-US07521
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                                                                                                                                                                                                                                                                                                                                                                          ЯC
                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0125683.
99US-0126522.
99US-0135169.
99US-0147383.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           s factor-receptor related protein;
.2-p36.3; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                             Ľ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Signal peptide"
39..283
/label= "TR2 recentor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                 Gentz
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                                                                                                       373pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              283
                                                                                                           English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ₿
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This invention relates to an isolated nucleic acid molecule encoding a human tumour necrosis factor(TNF)-receptor related protein TR2. Included in the invention are the two splice variants of TR2, TR2-SV1 and TR2-SV2 The TR2 gene is located on chromosome 1 at position p36.2-p36.3. TR2 is a

, TR2-SV1 and p36.2-p36.3.

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RESULT
AAY93695
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C Ireatment of aftericis or infinimulation using an antibody universe against CC a fragment of the TR2 protein. TR2 its agonists, antiagonists and CC immunosuppressive, antiallergic, antiarthritic, antianaemic, CC antibodies exhibit cytostatic, dermatological, antianaemic, CC antibodies exhibit cytostatic, dermatological, antianaemic, and CC cerebroprotective activity. The methods are useful for treating arthritis CC or inflammation, cancer (such as follicular lymphomas, carcinoma with p53 CC mutations, cardiac tumours, pancreatic, breast, or prostate cancer), an CC immunodeficiency or for enhancing an in vivo leukocyte response to an CC immunodeficiency or encephalomyelitis, rheumatoid arthritis, asthma, and CC inflammatory myopathies) and immunodeficiency disorders (such as actoimmune haemolytic anaemia, CC inflammatory myopathies) and immunodeficiency disorders (such as severely CC combined immunodeficiency (SCID) x linked, B cell lymphoproliferative CC inflammatory myopathies) and immunodeficiency with Igs). TR2, CC TR2-SV1 and/or TR2-SV2 polynucleotides and polypeptides, agonists or CC antagonists are useful for treating or preventing autolimmune diseases and CC inhibit the growth, progression and/or metastasis of cancers. They are CC also used to activate, differentiate or proliferate cancerous cells or CC insues, and can be used to treat diseases associated with increased cell survival, or the inhibition of apoptosis, e.g. Alzheimer's disease, CC Parkinson's disease, or Crohn's diseases. The TR2 polypeptides are useful CC as sources for generating antibodies, as molecular weight markers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                    Homo sapiens
                                                                                                                                             PRO201; PRO292; PRO327; PRO1265; PRO344; PRO343; PRO347; PRO357; PRO715; PRO1017; PRO1112; PRO509; PRO853; PRO882; tumour cell;
                                                                                                                                                                                                                                                    03-OCT-2000
                     Peptide
                                                                                                                                                                                                      Amino acid sequence of novel polypeptide PRO509
                                                                                                                                                                                                                                                                                                                                  AAY93695 standard;
                                                                                                                        tumourigenesis; cancer; neoplastic cell growth;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             member of the TNFR superfamily. The invention includes a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        treatment of arthritis or inflammation using an antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                       241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 100 les 283; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sources for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CSPGHFCIVQDGDHCAACRAYATSSPGQRVQKGGTESQDTLCQNCPPGTFSPNGTLEECQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VQRKRQEAEGEATVIEALQAPPDVTTVAVEETIPSFTGRSPNH 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HQTKCSWLVTKAGAGTSSSHWVWWFLSGSLVIVIVCSTVGLIICVKRRKPRGDVVKVIVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YRVKEACGELTGTVCEPCPPGTYIAHLNGLSKCLQCQMCDPAMGLRASRNCSRTENAVCG
                                                                                                                                                                                                                                                                                                                                                                                                                                   vqrkrqeaegeatviealqappdvttvaveetipsftgrspnh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hqtkcswlvtkagagtssshwvwwflsgslvivivcstvgliicvkrrkprgdvvkvivs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               \verb|cspghfcivqdgdhcaacray| atsspgqrvqkggtesqdtlcqncppgtfspngtleecq| \\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             yrvke \verb|acgeltgtvcepcppgtyiahlnglskclqcqmcdpamglrasrncsrtenavcg|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                        283
                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    generating antibodies, as molecular weight markers represents the TR2 receptor protein of the invention
/note= "signal sequence"
                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                Protein; 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 1578; DB 21; 100.0%; Pred. No. 4.5e-121;
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                                                                                                                      cell proliferation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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1 MEPPGDWGPPPWRSTPRTDVLRLVLYLTFLGAPCYAPALPSCKEDEYPVGSECCPKCSPG 60

Matches 283; Query Match Best Local Similarity

Conservative

0;

100.0%;

Score 1578; DB 21; Pred. No. 4.5e-121; ; Mismatches 0;

Indels Length

0,

Gaps

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08-MAR-1999;
02-JUN-1999;
                             The present sequence represents a novel human polypeptide. The specification describes novel polypeptides designated PRO201, PRO292, PRO377, PRO1265, PRO344, PRO343, PRO347, PRO357, PRO715, PRO1017, PRO1112, PRO509, PRO853 and PRO882. These genes are amplified in the genome of tumour cells. The polypeptides are believed to contribute to tumourigenesis. The polypeptides are useful target for the prognosis of tumour cancers, and may act as predictors of the prognosis of tumour treatment. Antibodies against these polypeptides are useful in the treatment and diagnosis of neoplastic cell growth
Sequence
                    and proliferation in
                                                                                                                                            Claim 61; Fig
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N-PSDB; AAA46931.
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 283 AA;
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99WO-US05028.
99WO-US12252.
99WO-US20111.
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99WO-US28313.
99WO-US28409.
99WO-US28301.
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193..1
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                                                                                                                                                                                                                                                           PRO509; human; antitumour; tumour; therapy; cytostatic; breast cancer; ovarian cancer; renal cancer; colorectal cancer; uterine cancer; prostate cancer; lung cancer; bladder cancer; central nervous system cancer; melanoma; leukaemia; neoplasm.
                                                                                                                                                                                                                                                                                            Human PRO509 antitumour protein.
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173..177
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153..159
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120..126
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192..201
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89..95
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193..1
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/note= "transmembrane domain"
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                                                        "Asn is N-glycosylated"
                                                                                  "N-myristoylation"
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08-MAR-1999;
21-APR-1999;
28-APR-1999;
14-MAY-1999;
20-JUL-1999;
26-JUL-1999;
15-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is that of human antitumour protein PRO509, as deduced from a retinal cDNA clone (see AAA49727). PRO509 shows homology to members of the human tumour necrosis factor receptor family such as the lymphotoxin-beta receptor (11 identities) and CD40 (12 identities). A claimed method for inhibiting the growth of a tumour cell comprises exposing the tumor cell to PRO179, PRO207, PRO320, PRO219, PRO221, PRO221, PRO2256, PRO326, PRO326, PRO326, PRO326, PRO326, PRO327, PRO327, PRO327, PRO327, PRO327, PRO327, PRO328, PRO509 or PRO866 (see AAY95337-49), their agonists cohimeric polypeptides incorporating them. The tumour is especially a cancer selected from breast, ovarian, renal, colorectal, uterine,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             prostate, lung, bladder and central nervous system cancer, melanoma and leukaemia. Methods for the recombinant expression of the antitumour proteins are also provided.
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99WO-US21090.
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99WO-US05028.
99US-0130232.
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99US-0144758.
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d WI;
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                                                                                                                                                             The human tumour necrosis factor (TNF) receptor related protein (TR2) is a member of the TNF family and displays considerable homology to murine CD40. It can be used in soluble forms to treat herpes simplex virus infection and TR2 proteins (or their agonists or antagonists) are used to treat disease associated with aberrant cell survival. Agonists may also be used to protect against the effects of radiation therapy and to stimulate lymphocyte proliferation and differentiation in patients infected by human immune deficiency syndrome.
                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                  Claim 1; Fig 1; 151pp; English.
                                                                                                                                                                                                                                                                                         simplex infection
                                                                                                                                                                                                                                                                                                 Nucleic acid encoding TR2 tumour necrosis factor family receptor and its splice variants, useful for diagnosis and treatment of diseases involving abnormal cell survival or death, e.g. herpes
                                                                                                                                                                                                                                                                                                                                                                               Gentz
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DB; AAV34509.
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yrvkeacgeltgtvcepcppgtyiahlnglskclqcqmcdpamglrasrncsrtenavcg
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                                                                                        Conservative
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Pred. No. 8e-121;
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lymphocyte proliferation;
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Similarity

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Conservative

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Score 1575; DB 2 Pred. No. 8e-121; l; Mismatches

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                                      This sequence represents the human tumour necrosis factor (TNF) receptor-like 2 (TR2) protein. Antibodies that target the TR2 protein can be used in the method of the invention to treat pathological conditions. The method is used to treat systemic lupus erythematosus, idiopathic thrombocytopaenic purpura, rheumatoid arthritis, multiple sclerosis, psoriasis, inflammatory bowel disease, insulin-dependent diabetes mellitus, allergic disorders, e.g. asthma, allergic rhinitis and atopic dermatitis, cancer, e.g. lymphomas and leukaemias, artherosclerosis and viral infections, e.g. Herpes simplex virus and AIDS. The TR2 antibody is also used to monitor and diagnose abnormalities in TR-2 function,
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     systemic lupus erythematosus; idiopathic thrombocytopaenic purpura; rheumatoid arthritis; multiple sclerosis; inflammatory bowel disease; insulin-dependent diabetes mellitus; allergic disorder; cancer; therapy;
                              production
                                                                                                                                                                                                                Disclosure; Page 27-28; 35pp; English.
                                                                                                                                                                                                                                             Method of treating pathological condition - tumour necrosis factor-2 antibody to patient
                                                                                                                                                                                                                                                                                                                                        Harrop JA,
                                                                                                                                                                                                                                                                                                                                                                                                                   12-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          artherosclerosis; viral infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tumour necrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human tumour necrosis factor receptor-like 2 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-MAR-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9851346-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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DB; AAV83763.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CSPGHFCIVQDGDHCAACRAYATSSPGQRVQKGGTESQDTLCQNCPPGTFSPNGTLEECQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HQTKCSWLVTKAGAGTSSSHWVWWFLSGSLVIVIVCSTVGLIICVKRRKPRGDVVKVIVS 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vqrkrqeaegeatviealqappdvttvaveetipsftgrspnh
                            or metabolism.
283
                                                                                                                                                                                                                                                                                                                                        Holmes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     factor receptor-like 2; TR2; TNF; human;
                                                                                                                                                                                                                                                                                                                                                                       BEECHAM PLC
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                                                                                                                                                                                                                                              to patient
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                                                                                                                                                                                                                                                              comprises administering
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26-MAR-1999;
20-MAY-1999;
                                                                                                         (NIJJ/)
(ROSE/)
                                                                                                                                                                                                                                                         Domain
                                                                                                                                                                                                                                                                                               Domain
                                                                                                                                                                                                                                                                                                                                                                                  chromosome p36.2-p36.3; arthritis; inflammation; autoimmune disease; immunodeficiency; metastasis; haemolytic anaemia; asthma; x-linked SCID; severely combined immunodeficiency; apoptosis inhibition; Alzheimer's disease; Parkinson's disease; Crohn's disease.
      Nucleic acid molecule encoding a human tumor necrosis factor and its two splice variants, useful for treating arthritis inflammation, cancer (such as follicular lymphomas) and
                                                                             Ni J,
                                                                                                                                      06-AUG-1999;
                                                                                                                                                                                     22-MAR-2000;
                                                                                                                                                                                                         28-SEP-2000.
                                                                                                                                                                                                                            WO200056405-A2
                                                                                                                                                                                                                                                                           Domain
                                                                                                                                                                                                                                                                                                                 Protein
                                                                                                                                                                                                                                                                                                                                                Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Human TR2-receptor protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY94717;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY94717 standard; Protein;
immunodeficiency disorders
                                                                                               (GENT/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            \verb|meppgdwgpppwrstpktdvlrlvlyltflgapcyapalpsckedeypvgseccpkcspg|
                                                                            Rosen CA,
                                                                                               ROSEN
GENTZ
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99US-0126522.
99US-0135169.
99US-0147383.
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                                                                                                                                                                                                                                                        /note=
226..2
                                                                                                                                                                                                                                                                                              /label= "TR2 receptor" 37..200
                                                                                                                                                                                                                                                                                                                 /note= "Signal peptide" 37..283
                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                    /note=
                                                                             Gentz
                                                                                                                                                                                                                                                                          ..225
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                                                                                                                                                                                                                                                                                   "Extracellular domain"
                                                                                                                                                                                                                                              "Intracellular domain"
                                                                                                                                                                                                                                                                 "Transmembrane domain"
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                           factor receptor
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cc earthinflammatory, nuturities, including the control of antiinflammatory, naturation, and ccrebroprotective activity. The methods are useful for treating arthritis cor inflammation, cancer (such as follicular lymphomas, carcinoma with p53 cc mutations, cardiac tumours, pancreatic, breast, or prostate cancer), an climmunodeficiency or for enhancing an in vivo leukocyte response to an antigen. Anti-TR2 antibodies are useful for treating, inhibiting or comprehenting autoimmune diseases (such as autoimmune haemolytic anaemia, dc dermatitis, allergic encephalomyelitis, rheumatoid arthritis, asthma, and combined immunodeficiency (SCID)-X linked, B cell lymphoproliferative combined immunodeficiency (SCID)-X linked, B cell lymphoproliferative combined immunodeficiency combined immunodeficiency with Igs). TR2, TR2-SV1 and/or TR2-SV2 polynucleotides and polypeptides, agonists or antagonists are useful for treating or preventing autoimmune diseases and linhibit the growth, progression and/or metastasis of cancers. They are calso used to activate, differentiate or proliferate cancerous cells or tissues, and can be used to treat diseases associated with increased cell survival, or the inhibition of apoptosis, e.g. Alzheimer's disease, cell as sources for generating antibodies, as molecular weight markers.

CC This sequence represents the TR2 receptor protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a fragment of the TR2 protein. TR2 its agonists, antagonists and antibodies exhibit cytostatic, dermatological, antianaemic, immunosuppressive, antiallergic, antiarthritic, antiasthmatic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The TR2 gene is located on chromosome 1 at position p36.2-p36.3. TR2 is a member of the TNFR superfamily. The invention includes a method for the treatment of arthritis or inflammation using an antibody directed against
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention relates to an isolated nucleic acid molecule encoding a human tumour necrosis factor(TNF)-receptor related protein TR2. Included in the invention are the two splice variants of TR2, TR2-SV1 and TR2-SV2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1;
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      283 AA;
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Best Local
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           VQRKRQEAEGEATVIEALQAPPDVTTVAVEETIPSFTGRSPNH
                                            CSPGHFCIVQDGDHCAACRAYATSSPGQRVQKGGTESQDTLCQNCPPGTFSPNGTLEECQ
                                                                                                                                                       YRVKEACGELTGTVCEPCPPGTYIAHLNGLSKCLQCQMCDPAMGLRASRNCSRTENAVCG
                                                                                                                                                                                                      MEPPGDWGPPPWRSTPRTDVLRLVLYLTFLGAPCYAPALPSCKEDEYPVGSECCPKCSPG
v {\tt qrkrqeaegeatviealqappdvttvaveetipsftgrspnh}
                                                                                                                                                                                         meppgdwgpppwrstpktdvlrlvlyltflgapcyapalpsckedeypvgseccpkcspg
                                                                     HQTKCSWLVTKAGAGTSSSHWVWWFLSGSLVIVIVCSTVGLIICVKRRKPRGDVVKVIVS
                                                                                                                                           yrvkeacgeltgtvcepcppgtyiahlnglskclqcqmcdpamglrasrncsrtenavcg
                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                     99.8%;
                                                                                                                                                                                                                                                     Score 1575; DB 21; Pred. No. 8e-121;
                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                         0;
                       283
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                                                                                                                                                                                                                                                                 Length
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                                                                                                                                                                                                                                         Gaps
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AAW95031
                    Tumour necrosis factor receptor (TNF-R) related polypeptide
                                    13-MAY-1999
                                                                  AAW95031
                                                                standard; protein;
                                   (first entry)
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Tumour necrosis factor receptor; TNF-R;

TR1; TR2; TL2;

transplant rejection;

TL4;

TR2.

inflammation; septicemia; autoimmune disease;

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                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to identifying agonists or antagonists to tumour necrosis factor receptor (TNN-R) related polypeptides (TR1 and TR2, TL2 and TL4). The method comprises: (a) (i) contacting TR1 or TR2 with a candidate compound in the presence of TL2 or TL4; or (ii) contacting TR1 or TR2; and (b) assessing the ability of the candidate compound to compete with TR1 or TR2 binding to TL2 or TL4. TR and TL agonists and antagonists are useful for treating diseases caused by imbalance of TL or TR polypeptide levels, which cause: chronic and acute inflammation, arthritis, septicemia, autoimmune diseases, transplant rejection, graft vs. host disease, infection, stroke, ischemia, acute respiratory disease syndrome, restenosis, brain injury, AIDS, bone diseases, cancer, athersclerosis and Alzheimer's disease. The present sequence represents a TNF-R related polypeptide TR2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-AUG-1997;
13-AUG-1997;
26-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              graft vs. host disease; infection; stroke; ischemia; brain injury; AIDS; acute respiratory disease syndrome;, restenosis, bone disease; cancer; athersclerosis; Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identifying agonists and antagonists to tumour necrosis factor receptor (TNF-R) related polypeptides (TR1, TR2, TL2 and TL4) useful for treating stroke, Alzheimer's disease and AIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 13-14; 18pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brigham-burke MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-JUN-1998;
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nes 282; Conserv
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                                                                                                            VQRKRQEAEGEATVIEALQAPPDVTTVAVEETIPSFTGRSPNH
                                                      HQTKCSWLVTKAGAGTSSSHWVWWFLSGSLVIVIVCSTVGLIICVKRRKPRGDVVKVIVS
                                                                                                                                                                     MEPPGDWGPPPWRSTPRTDVLRLVLYLTFLGAPCYAPALPSCKEDEYPVGSECCPKCSPG
vqrkrqeaegeatviealqappdvttvaveetipsftgrspnh
                                                                                                                                                                                                   YRVKEACGELTGTVCEPCPPGTYIAHLNGLSKCLQCQMCDPAMGLRASRNCSRTENAVCG 120
                                                                                                                                                                                                                                                                                                                                                                  283 AA;
                                                                                                                                                                                                                                                                                           Conservative
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97US-0055513.
97US-0056980.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Young
                                                                                                                                                                                                                                                                                                     99.68;
                                                                                                                                                                                                                                                                                                     Score 1572; DB 20;
Pred. No. 1.4e-120;
                                                                                                                                                                                                                                                                                         Mismatches
 283
                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                      283;
                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                      Gaps
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RESULT AAW12659

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Human herpes simplex virus (HSV) cellular mediator (HVEM) (AAW12659) is a novel member of the TNF/MGF receptor family that mediates or enhances entry of HSV into cells. Its amino acid sequence was deduced from a cDNA clone (AAT51737) isolated from an HeLa library by its ability to convert CHO-KI cells from resistance to susceptibility to HSV-1 entry. Recombinant HVEM can be produced in bacterial or mammalian (esp. CHO) cells. It can be used as an immunoassay reagent to detect specific antibodies, to screen for
                                                                                                                                                                                                  New human herpes simplex virus cellular mediator - used for diagnosis, drug screening and therapeutically to inhibit entry HSV into cells
                      drugs having an (ant)agonist effect on HSV entry into cells, generate antibodies, to screen for the (currently unknown) H ligand, and to identify inhibitors of HSV-HVEM interaction.
                                                                                                                                                                         Claim 1; Fig 2; 54pp;
                                                                                                                                                                                                                                                  WPI; 1997-145273/13.
N-PSDB; AAT51737.
                                                                                                                                                                                                                                                                                        Montgomery RI,
                                                                                                                                                                                                                                                                                                                (NOUN ) UNIV NORTHWESTERN
                                                                                                                                                                                                                                                                                                                                                                 26-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diagnosis; agonist; antagonist; antibody.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Herpes simplex virus cellular mediator; HVEM; receptor; HSV;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide
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                                                                                                                                                                                                                                                                                                                                          95US-0509024.
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110..112
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42..75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "potential N-glycosylation site" 173..175
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                                                                                                                                                                         English.
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  of TNF/NGF receptor family"
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                                                                                                                                                 cellular mediator (HVEM) (AAW12659)
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virus (HSV) entry mediator that is a member of the tumour necrosis factor receptor family, and which confers on HSV the ability to infect and replicate in otherwise non-permissive cells. In the present invention, the combination of a novel porcine cell model system which is refractory to HCV entry, along with specific HSV B5 (see AAY05796) and/or HVEM receptor proteins enables the development of assays for screening antiviral compounds and therapeutics. The assays are useful for detecting the ability of agents to inhibit HSV entry or spread and provide for facile high-throughput screening of compounds suspected to be able to inhibit such entry, e.g. compound libraries, peptide libraries etc., to identify
                                                                                                                                                                                                                                   The present sequence represents HVEM, a novel human herpes simplex
                                                                                                                                                                                                                                                                         Claim 10; Page 71-72; 89pp; English.
                                                                                                                                                                                                                                                                                                                    Human herpes simplex virus
                                                                                                                                                                                                                                                                                                                                                             N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-302740/25.
                                                                                                                                                                                                                                                                                                                                                                                                                           Fuller AO,
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99.3%;
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Pred. No. 2e-120;
1; Mismatches 1;
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Best Local
                                                                                                                                                                                                                                                                                                                                                  mHVEM-2; membrane-bound herpesvirus entry mediator-2; TANGO-69-receptor; tumour necrosis factor receptor; herpes simplex virus; infection; cancer; inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              potential drug candidates. The comprising the HSV receptor, fragments of the polypeptide
16-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY79207 standard;
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                                                            Modified-site
                                                                                     Modified-site
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                                                                                                                                                                                                                                                   Protein
                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                       autoimmune disorder; therapy; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                   Membrane-bound
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                   herpesvirus
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                                                                                                                                                                                      /note= "
78..119
                                                            /note= "N-glycosylated"
173
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                                                                                                             /note=
201..2
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39..277
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                                                                                                                                                                                                "cysteine-rich domain"
                                                                                                                                                                        "cysteine-rich domain"
                                                                                                                                                                                                                                                              "signal peptide"
                                                "N-glycosylated"
                                                                                                                       "cysteine-rich domain (partial)"
                                                                                                                                                 "cysteine-rich domain"
                                                                                                                                                                                                                          "mature protein, also separately claimed in Claim \boldsymbol{8}\text{ }^{\text{n}}
                                                                                              "transmembrane domain"
                                                                                                                                                                                                                                                                                                                                                                                                   entry mediator-2 (mHVEM2).
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Pred. No. 2
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                           Matches 245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   disrupted. DNA encoding HVEM, HVEM proteins and HVEM antibodies can be used in screening and detection assays (e.g., chromosomal mapping, tissue typing). HVEM proteins can also be used for regulation of cell proliferation, cell differentiation, cell survival, inflammation mast cell activity, HSV infection and/or proliferation, and/or coagulation. HVEM agonists can be used to treat disorders associated with decreased HVEM activity, e.g. proliferative disorders such as carcinoma or pathogenic infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (see AAZ94198). mHVEM2 is a TANGO-69-receptor and member of the tumour necrosis factor receptor (TMFR) superfamily. HVEM plays a role in herpes simplex virus (HSV) entry. The invention is based on the discovery of 3 cDNA molecules (see AAX94195-97) which encode soluble forms (see AAY79204-06) of mHVEM, and the cDNA molecule encoding of mHVEM2. In addition to isolated full-length proteins and polynucleotides, and invention provides TANGO-69-receptor fusion proteins, antigenic peptides and antibodies. Also provided are recombinant expression vectors, host cells and transgenic animals in which a TANGO-69-receptor gene has been introduced or the provided of the provided are recombinant expression vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               is human membrane-bound herpesvirus entry mediator-2 (mHVEM2), a novel form of membrane-bound herpesvirus entry mediator (mHVEM), novel form of membrane-bound herpesvirus entry mediator (mHVEM). The amino acid sequence was deduced from an isolated cDNA clone (see AAZ94198), mHVEM2 is a TANGO-69-receptor and member of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New nucleic acid molecule encoding herpes virus entry mediator (HVEM), either in the soluble or membrane bound form, is useful in screening assays and detection assays \cdot
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29-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antagonists can be used to treat disorders associated with increased HVEM activity, e.g. autoimmune, T cell, inflamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This polypeptide, the mature portion of which is also claimed,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MILL-) MILLENNIUM BIOTHERAPEUTICS INC
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                                       241
                                                                               181
                                                                                                                       181
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                                                                                                                                                                                                                                                                                                                                            1 MEPPGDWGPPPWRSTPRTDVLRLVLYLTFLGAPCYAPALPSCKEDEYPVGSECCPKCSPG
                                                                                                                                                                               CSPGHFCIVQDGDHCAACRAYATSSPGQRVQKGGTESQDTLCQNCPPGTFSPNGTLEECQ 180
                                                                                                                                                                                                                                                               YRVKEACGELTGTVCEPCPPGTYIAHLNGLSKCLQCQMCDPAMGLRASRNCSRTENAVCG 120
                                                                                                                                                                                                                                                                                                                       \verb|meppgdwgpppwrstprtdvlrlvlyltflgapcyapalpsckedeypvgseccpkcspg|
vq-----vlillplslpp
                                       VQRKRQEAEGEATVIEALQAPP
                                                                           yrvkeacgeltgtvcepcppgtyiahlnglskclqcqmcdpamglrasrncsrtenavcg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000-256981/22.
)B; AAZ94198.
                                                                                                                       HQTKCSWLVTKAGAGTSSSHWVWWFLSGSLVIVIVCSTVGLIICVKRRKPRGDVVKVIVS
                                                                                                                                                        cspghfcivqdgdhcaacrayatsspgqrvqkggtesqdtlcqncppgtfspngtleecq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                inflammation disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fig 7; 149pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-0146950
99US-0342767
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                                                                                                                                                                                                                                                                                                                                                                                                                         87.0%;
93.5%;
                                       262
                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1373.5; DB 21; Pred. No. 2.1e-104;
                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 inflammatory and
                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                              277;
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C (see AAZ94195). SHVMNI is a TANGO-69-receptor and members of the tumour necrosis factor receptor (TNFR) superfamily. It is thought to play a role analagous to other soluble members of the thought to play a role analagous to other soluble members of the TNFR superfamily by interfering with the ability of LIGHT-TANGO-69 and lymphotoxin to bind mHVEM, and to play a role in herpes simplex virus (HSV) entry. The invention is based on the discovery of 3 CCDNA molecules (see AAZ94195-97) which encode soluble forms (see CCDA, molecules (see AAZ94195-97), of mHVEM. In addition to isolated full-length proteins and polynucleotides, and invention CC isolated full-length proteins and polynucleotides, and invention CC provides TANGO-9-receptor fusion proteins, antigenic peptides and CCC antibodies. Also provided are recombinant expression vectors,
                 X S X
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                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid molecule encoding herpes virus entry mediator (HVEM), either in the soluble or membrane bound form, is useful in screening assays and detection assays - \,
                                                                                                                                                                                                                                                                                                               This polypeptide, the mature portion of which is also claimed, is human soluble herpesvirus entry mediator-1 (sHVEM1), a novel soluble form of membrane-bound herpesvirus entry mediator (mHVE
                                                                                                                                                                                                                                                                       The amino acid sequence was deduced from an isolated cDNA clone (see AAZ94195). SHYEM1 is a TANGO-69-receptor and member of the
                                                                                                                                                                                                                                                                                                                                                                                                     Claim 8; Fig 1; 149pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-256981/22
N-PSDB; AAZ94195.
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29-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MILL-) MILLENNIUM BIOTHERAPEUTICS INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      infection; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SHVEM-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Soluble herpesvirus entry mediator-1 (sHVEM1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-JUN-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            eptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                soluble herpesvirus entry mediator-1; TANGO-69-receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-0146950
99US-0342767
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110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   factor receptor; human; herpes simplex
er; inflammation; autoimmune disorder; t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note=."N-glycosylated"
173
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1..36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "cysteine-rich domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "mature protein, also separately claimed in Claim 8" \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "cysteine-rich domain"
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AAY7920X
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XX AAY7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sHVEM-2; soluble herpesvirus entry mediator-2; TANGO-69-receptor; tumour necrosis factor receptor; human; herpes simplex virus; infection; cancer; inflammation; autoimmune disorder; therapy;
                                                                                                                                Modified-site
                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                   Domain
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                                                                                                                                                                                                                                                                                   /note= '78..119
                                                                                                                                                                                /note=
110
                                                                                                                                /note= "N-glycosylated"
173
                                                                                                                                                                                                                                /note= "c
121..162
                                                                                                                                                                                                                                                                                                                                                                                                              /note= "signal peptide"
39..197
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                                                                                                  "N-glycosylated
                                                                                                                                                                                                                                                                                                           "cysteine-rich domain"
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                                                                                                                                                                                                        "cysteine-rich domain"
                                                                                                                                                                                                                                                                                                                                                             "mature protein, also separately claimed
in Claim 8"
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Pred. No. 1.2e-79;
1; Mismatches 2;
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Qy В

CSPGHFCIVQDGDHCAACRAYATSSPGQRVQKGGTESQDTLCQNCPPGTFSPNGTLEECQ

180 120 120

cspghfcivqdgdhcaacrayatsspgqrvqkggtesqdtlcqncppgtfspngtleecq

YRVKEACGELTGTVCEPCPPGTYIAHLNGLSKCLQCQMCDPAMGLRASRNCSRTENAVCG

yrvkeacgeltgtvcepcppgtyiahlnglskclqcqmcdpamglrasrncsrtenavcg

οy B Qy

61 61 Query Match Best Local Similarity

67.2%; 98.4%;

Score 1060; DB 2 Pred. No. 5.4e-79 Mismatches

DB 21; 0;

Length 197; Indels

2;

Gaps

1;

60 60

Matches

184;

Conservative

1;

MEPPGDMGPPPMRSTPRTDVLRLVLYLTFLGAPCYAPALPSCKEDEYPVGSECCPKCSPG

meppgdwgpppwrstprtdvlrlvlyltflgapcyapalpsckedeypvgseccpkcspg

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hqt--nw HQTKCSW 187

185

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The anticours of the Common transfer of the CC thought to play a role analagous to other soluble members of the CC TMFR superfamily by interfering with the ability of LIGHT-TANGO-69 CC TMFR superfamily by interfering with the ability of LIGHT-TANGO-69 CC and lymphotoxin to bind miyEM, and to play a role in herpes simplex virus (HSV) entry. The invention is based on the discovery of 3 CC cDNA molecules (see AAZ94195-97) which encode soluble forms (see AAY9204-66), and I cDNA molecule (see AAZ94198) that encodes a 2nd membrane-bound form (see AAY79207), of mHVEM. In addition to consisted full-length proteins and polynucleotides, and invention CC provides TANGO-69-receptor fusion proteins, antipenic epetides and committees and transgenic animals in which a TANGO-69-receptor gene has been introduced or disrupted. DNA encoding HVEM, HVEM commonsomal mapping, tissue typing). HVEM proteins and HVEM antibodies can be used in screening and detection assays (e.g. chromosomal mapping, tissue typing). HVEM proteins can also be used for regulation of cell proliferation, cell activity, cell survival, inflammation mast cell activity, cell sound for proliferation, and/or coagulation. HVEM activity, e.g. proliferative disorders such as carcinoma or cassociated with increased HVEM activity, e.g. autoimmune, T cell, inflammatory and allergic inflammation disorders.
  is human soluble herpesvirus entry mediator-2 (sHYEM2), a novel soluble form of membrane-bound herpesvirus entry mediator (mHYEM The amino acid sequence was deduced from an isolated cDNA clone (see AAZ34196). sHYEM2 is a TANGO-69-receptor and member of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acid molecule encoding herpes virus entry mediator (HVEM), either in the soluble or membrane bound form, is useful in screening assays and detection assays - {\sf var}
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This polypeptide, the mature portion of which is also claimed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 8; Fig 3; 149pp; English.
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29-JUN-1999;
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  197 AA;
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99US-0342767
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Search completed: January 24, 2002, 16:21:43
Job time: 33 sec

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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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2: /cgn2_6/ptodata/2,
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PCT-US96-12374-2
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US-09-146-950-12
US-09-146-950-25
US-09-146-950-25
US-09-146-950-25
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US-09-042-785A-10
US-09-042-785A-17
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US-08-795-447A-47
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US-08-795-446B-47
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US-08-974-126-47
US-08-974-126-48
US-09-042-785A-9
PCT-US91-02207-9
PCT-US91-02207-9
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RESULT 2
US-09-33-279-2
; Sequence 2, Application US/09333279
; Patent No. 6303336
; GENERAL INFORMATION:
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HQTKCSWLYTKAGAGTSSSHWVWWFLSGSLVIVIVCSTVGLIICVKRRKPRGDVVKVIVS 	RVKEACGELTGTVCEPCPPGTYIAHLNGLSKCLQCQMCDPAMGLRASRNCSRTENAVC	tch 100.0%; Score 1578; DB 4; Lengt al Similarity 100.0%; Pred. No. 2.5e-134; 283; Conservative 0; Mismatches 0; Indel MEPPGDWGPPPWRSTPRTDVLRLVLYLTFLGAPCYAPALPSCKEDEYPVG	D8-795 D8-385 D8-385 D8-385 D8-650 D9-004 D8-477 D8-477 D8-243 D8-974 D8-974 D8-974 D8-974 D8-795 D8-795 D8-476 D8-476 D8-476 D8-476 D8-476 D8-476 D8-476 D8-476 D8-795 D8-476	
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/VKVIV	CSRTENAVCG CSRTENAVCG SPNGTLEECQ	3; 0; PKCSI 	sequence	
S 240 S 240	G 120 G 120 G 180 Q 180 Q 180	Gaps Gaps 60	48, Appli 2, Appli 7, Appli 4, Appli 4, Appli 4, Appli 4, Appli 49, Appli 49, Appli 49, Appli 7, Appli	

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APPLICANT: SPEAR, Patricia G.
APPLICANT: MONTGOMERY, Rebecca I.
TITLE OF INVENTION: HERPES VIRUS ENTRY RECEPTOR PROTEIN
FILE REFERENCE: 0290-1
CURRENT APPLICATION NUMBER: US/09/333,279
CURRENT FILING DATE: 1999-06-15
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
SEQ ID NO 2
LENGTH: 283
TYPE: PRT
OGRANISM: Homo sapiens
US-09-333-279-2
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Best Local Similarity
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                               CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Northrup, Thomas E.
REGISTRATION NUMBER: 33,268
REFERENCE/DOCKET NUMBER: NOR3446P020PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 616-5400
                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/12374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Northwestern University
TITLE OF INVENTION: Herpes Virus Entry Mediator
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
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7: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                      180 N. Stetson,
                                                                      (312) 616-5460
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Goldsmith, Milnamow on, Suite 4700
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                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: SPEAR, PARTICIA G.
APPLICANT: MONTGOMERY, Rebecca I.
APPLICANT: MONTGOMERY HERPES VIRUS
                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 419
TYPE: PRT
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                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/08/509,024B CURRENT FILING DATE: 1995-07-25 NUMBER OF SEQ ID NOS: 7
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Busfield, Samantha J.
FILE OF INVENTION: NOVEL MOLECULES OF THE HE
FILE OF INVENTION: PROTEIN FAMILY AND USES T
FILE REFERENCE: 09404/057001
CURRENT APPLICATION NUMBER: US/09/146,950A
CURRENT FILING DATE: 1998-09-03
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
SEQ ID NO 2
LENGTH: 193
TYPE: PRT
ORGANISM: Homo sapiens
US-09-146-950-2
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CURRENT APPLICATION NUMBER: US/09/333,279

CURRENT FILING DATE: 1999-06-15

NUMBER OF SEQ ID NOS: 7

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 7

LENGTH: 419

TYPE: PRT

ORGANISM: Homo sapiens
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Best Local S
Matches 184
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Best Local
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APPLICANT: SPEAR, Patricia G.

APPLICANT: MONTGOMERY, Rebecca I.

TITLE OF INVENTION: HERPES VIRUS ENTRY RECEPTOR PROTEIN
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                                                             MEPPGDMGPPPMRSTPRTDVLRLVLYLTFLGAPCYAPALPSCKEDEYPVGSECCPKCSPG 60
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98.4%;
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                                                                                                                                                            DB 4; Length 193;
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                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/09146950A Patent No. 6287808 GENERAL INFORMATION:
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 18
LENGTH: 197
TYPE: PRT
                                                                                                                                           SEQ ID NO 4
LENGTH: 155
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Best Local Similarity
Matches 184; Conserv
Query Match
Best Local Similarity
Matches 146; Conserv
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                                                                                                                                                                                                         APPLICANT: Busfield, Samantha J.
TITLE OF INVENTION: NOVEL MOLECULES OF THE HERDESVIRUS-ENTRY-MEDIATOR-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
FILE REFERENCE: 09404/057001
CURRENT APPLICATION NUMBER: US/09/146,950A
CURRENT FILING DATE: 1998-09-03
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                                                                                                                                                                                                 NUMBER OF SEQ ID NOS:
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                                                                                                                                                                                 SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                              TYPE: PRT
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98.4%;
                  53.7%;
 Score 847; DB 4;
Pred. No. 5.7e-69;
1; Mismatches 2
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Pred. No. 5.
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                                   Length 155;
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US-09-146-950-20
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SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 20
LENGTH: 159
                                                                                                                           NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 25
LENGTH: 77
                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Busfield, Samantha J.
                                                                                                                                                                                                                                                                                                                                     Sequence 25, Application US/09146950A Patent No. 6287808
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Query Match
Best Local Similarity
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Best Local Similarity
Matches 146; Conserv
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                                                                                                                                                                                                  TITLE OF INVENTION: NOVEL MOLECULES OF THE HERPESVIRUS-ENTRY-MEDIATOR-RELATED TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF FILE REFERENCE: 09404/057001
CURRENT APPLICATION NUMBER: US/09/146,950A
CURRENT FILING DATE: 1998-09-03
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TITLE OF INVENTION: NOVEL MOLECULES OF THE HERDESVIRUS-ENTRY-MEDIATOR-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
FILE REFERENCE: 09404/057001
                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
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Pred. No. 3.1e-68;
1; Mismatches C
Score 365; DB 4;
Pred. No. 4.9e-26;
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GENERAL INFORMATION:
APPLICANT: Busfield, Samantha J
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 289 amino acid
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FILING DATE: 17-MAR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
FILING DATE: 26-SEP-1997
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ADDRESSEE: LAHIVE & COCKFIELD, LLP
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FRAGMENT TYPE:
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ATTORNEY/AGENT INFORMATION:
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CURRENT APPLICATION DATA:
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TITLE OF INVENTION: NOVEL MOLECULES OF THE TNF RECEPTOR SUPERFAMILY
TITLE OF INVENTION: AND USES THEREFOR
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REGISTRATION NUMBER: 36,20
REFERENCE/DOCKET NUMBER: 1
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CITY: Boston
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CSTVGLIIC-----VKR--RKPRGDVVKVIVSVQRKRQEAEGEATVIEALQAPPDVTT 266
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                                                                                                                    VCHPCPVGFFSNQSSLFEKCYPWTSCEDKNLEVLQK---GTSQTNVICGLKSRMRALLVI 198
                                                                                                                                                                               LCQNCPPGTFSPNGTL-EECQHQTKCS----WLVTKAGAGTSSSHWVWWFLSGSLVIVIV 215
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 276 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815,
REFERENCE/DOCKET NUMBER: P-LJ 2626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Bredesen, Dale E.
APPLICANT: Rabizadeh, Sharroz
TITLE OF INVENTION: Prospoptotic Peptides, De
TITLE OF INVENTION: Polypeptides and Methods
NUMBER OF SEQUENCES: 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (619) 535-9001
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,886
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226
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                                                                                                                                                                                                                                                                                                                                                                      / Match 17.0%;
Local Similarity 26.1%;
nes 71; Conservative 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                     CAACRAYATSSPGQRVQKGGTESQDTLCQNCPPGTFS-PNGTLEECQHQTKCSW--LVTK 191
                                                                                                                                                                                                                                                  CEPCPPGTYIAHLNGLSKCLQCQMCDPAMGLRASRNCSRTENAVCGCSPGHFCIVQDGDH 134
                                                                                                                                              CESCVLHRSCSPGFGVKQIATGVSDTICEPCPVGFFSNVSSAFEKCHPWTSCETKDLVVQ 175
                                                                                                                                                                                                                                                                                                MVRLPLQCVLWG--CLLTAVHPEPPTACREKQYLINSQCCSLCQPGQKLVSDCTEFTETE 58
AP--HPKQEPQEINFPDDLPGSNTAAPVQETL 255
                                    ATVIEALQAPPDV---
                                                                         Q-AGTNKTDVVCGPQDRLRALVVIPIIFGILFA---
                                                                                                           AGAGTSSSHWVWWFLSGSLVIVIVCSTVGLIICVKRRKPRGDVVKVIVSVQRKRQEAEGE 251
                                                                                                                                                                                                                       CLPCGESEFLDTWNRETHCHQHKYCDPNLGLRVQQKGTSETDTICTCEEGWHC---TSEA 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           276 amino acids
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                                  -TTVAVEETI 273
                                                                                                                                                                                                                                                                                                                                                                      Score 267.5; DB 4;
Pred. No. 1.3e-16;
0; Mismatches 116;
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ds of Use
                                                                         -ILLVLVFIKKVAKKPTNK 225
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Best Local Similarity
Thes 71; Conserv
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GENERAL INFORMATION:
APPLICANT: Busfield, Samantha J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 17-MAR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/938
FILING DATE: 26-SEP-1997
AUTORNEY/AGENT INFORMATION:
NAME: MANDATATION NUMBER: 36,207
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MEI-
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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FRAGMENT TYPE:
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TELEPHONE: (617)227-7400
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TITLE OF INVENTION: NOVEL MOLECULES OF
TITLE OF INVENTION: AND USES THEREFOR
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226
                                                                      252
                                                                                                                                            176 Q-AGTNKTDVVCGPQDRLRALVVIPIIFGILFA--
                                                                                                                                                                                                                                                                                                116 CESCVLHRSCSPGFGVKQIATGVSDTICEPCPVGFFSNVSSAFEKCHPWTSCETKDLVVQ 175
                                                                                                                                                                                                                                                                                                                                   135 CAACRAYATSSPGQRVQKGGTESQDTLCQNCPPGTFS-PNGTLEECQHQTKCSW--LVTK 191 | :| :| | | | | : 1:1 | | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1:1 | : 1 | :
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CITY: I
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AP--HPKQEPQEINFPDDLPGSNTAAPVQETL 255
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                                                                  -TTVAVEETI 273
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RESULT 14 US-09-006-353A-10 ; Sequence 10, Application US/09006353A

Patent No. 6261801

GENERAL INFORMATION:

APPLICANT: WEI,

YING-FEI

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RESULT 15
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                                                     Sequence 47, Application US/08974022 Patent No. 6015938
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Best Local Similarity
                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (301) 309-85 INFORMATION FOR SEQ ID NO:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: PETELECOMMUNICATION INFORMATION: TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BROOKES, ANDERS A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/006,353A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: YU, GUO-LIANG
APPLICANT: GENTZ, REINER
APPLICANT: RUBEN, STEVEN
TITLE OF INVENTION: TUMOR NECROSIS FACTOR RECEPTOR
NUMBER OF SEQUENCES: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 277 amino acid
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                                                                                                                                                                       226
                                                                                                                                                                                                                                            176 Q-AGTNKTDVVCGPQDRLRALVVIPIIFGILFA---
                                                                                                                                                                                                                                                                              192 AGAGTSSSHWVWWFLSGSLVIVIVCSTVGLIICVKRRKPRGDVVKVIVSVQRKRQEAEGE 251
                                                                                                                                                                                                                                                                                                                                                      135 CAACRAYATSSPGQRVQKGGTESQDTLCQNCPPGTFS-PNGTLEECQHQTKCSW--LVTK 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: HUMAN
STREET: 9410 KEY
CITY: ROCKVILLE
                                                                                                                                                                                                                                                                                                                                                                                            59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                             75 CEPCPPGTYIAHLNGLSKCLQCQMCDPAMGLRASRNCSRTENAVCGCSPGHFCIVQDGDH 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 VLRLVLYLTFLGAPCYAPAL-----PSCKEDEYPVGSECCPKCSPGYRVKEACGELTGTV 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U
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                                                                                                                                                                     AP--HPKQEPQEINFPDDLPGSNTAAPVQETL 255
                                                                                                                                                                                                                                                                                                                 CESCVLHRSCSPGFGVKQIATGVSDTICEPCPVGFFSNVSSAFEKCHPWTSCETKDLVVQ
                                                                                                                                                                                                         ATVIEALQAPPDV-----TTVAVEETI 273
                                                                                                                                                                                                                                                                                                                                                                                          CLPCGESEFLDTWNRETHCHQHKYCDPNLGLRVQQKGTSETDTICTCEEGWHC---TSEA 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MVRLPLQCVLWG--CLLTAVHPEPPTACREKQYLINSQCCSLCQPGQKLVSDCTEFTETE
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9410 KEY WEST AVENUE
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Boyle,
Lacey,
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David L.
                   Willaim J.
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MRER: PF341
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Search completed: January 24, Job time: 52 sec

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Best Local Similarity
Matches 62; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 207 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                               180
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                                                                                                                                                                                                        177 LYPVNETSCT---TTAG 190
                                                                                                                                                                   118 NGCRIC-APQTKCPAGYGVSGHTRAGDTLCEKCPPHTYSDSLSPTERCGTSFNYISVGFN 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: LBM .. COMPUTER: LBM .. PC-DOS/MU .. OPERATING SYSTEM: PC-DOS/MU .. OPERATING SYSTE
                                                                                                                                                                                                                                                                                                                             60
                                                                                                                                                                                                                                                                                                                                                                           74 VCEPCPPGTYIAHLNGLSKCLQCQMCDPAMG-LRASRNCSRTENAVCGCSPGHFCIVQDG 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20 VLRLVLYLTFLGAPCYAPALP-----SCKEDEYPVGSECCPKCSPGYRVKEACGELTGT 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/0 FILING DATE: 12-DEC-1995
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                                                                               ---QHQTKCSWLVTKAG 193
                                                                                                                                                                                                                                                                                                                         VCSPCEDGTFTASTNHAPACVSCR--GPCTGHLSESQPCDRTHDRVCNCSTGNYCLLKGQ 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16.5%; Score 260; DB 3;
31.5%; Pred. No. 4.4e-16;
tive 25; Mismatches 80;
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  US-08-741-095B-26
1578
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Listing first 45 summaries
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Copyright (c) 1993 - 2000
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/cgn2_6/ptodata/2/paa/US06_COMB.pep:*
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Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ength	DB	ID	Description
283	_	PCT-US01-26396-31	Sequence 31, Appl
283	ب	PCT-US95-05058-2	Sequence 2, Appli
283	_	PCT-US99-20180-13	Sequence 13, Appl
283	œ	US-08-462-315-2	Sequence 2, Appli
283	8	US-08-462-962-2	Sequence 2, Appli
283	œ	US-08-464-595-2	Sequence 2, Appli
283	11	US-08-741-095B-26	Sequence 26, Appl
283	13	US-08-987-902-1	Sequence 1, Appli
283	17	US-09-342-767-13	Sequence 13, Appl
	283 283 283 283 283 283 283 283 283	1 DB 1 1 1 1 1 8 8 8 1 1 1 1 1 1 1 1	ength DB ID 283 1 PCT-US01-26396-31 283 1 PCT-US95-05058-2 283 1 PCT-US99-20180-13 283 8 US-08-462-315-2 283 8 US-08-462-562-2 283 8 US-08-464-595-2 283 11 US-08-741-0958-26 283 13 US-08-987-902-1 283 17 US-09-342-767-13

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56,	56,	56,	e 30,	30,	e 18,	18,	Sequence 2, Appli	2, 7	e 44,	44,	Sequence 42, Appl	42,	4,	2	2,	'n		874	73,	2	'n	2	2	26,	2		26,	2	e 2	2, AJ	31,	60,	Sequence 46, Appl	26,	reducing the polynomia

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PCT-US01-26396-31
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Sequence 31, Application PC/TUS0126396
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta; FILE REFERENCE: PF454PCT3
                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 31
  Query Match
Best Local Similarity
Matches 283; Conserv
                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: PCT/US01/26396
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: 60/303,224
PRIOR FILING DATE: 2001-07-06
PRIOR APPLICATION NUMBER: 60/252,131
PRIOR PRIOR PRIOR DATE: 2000-11-21
PRIOR PRIOR APPLICATION NUMBER: 60/227,598
PRIOR FILING DATE: 2000-08-25
                                                                                                                                                LENGTH: 283
TYPE: PRT
ORGANISM: Homo sapiens
100.0%; Score 1578; DB 1; ilarity 100.0%; Pred. No. 3.6e-119; Conservative 0; Mismatches 0;
                                                    Length 283;
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Best Local S
Matches 283
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ENFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                           STRANDEDNESS:
TOPOLOGY: LI
MOLECULE TYPE:
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MEDIUM TYPE: 3.5 INC
COMPUTER: IBM PS/2
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STREET: NEW JERSEY
STATE: NEW JERSEY
USA
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TITLE OF INVENTION: Tumor Necrosis Factor Receptors
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
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 61
                              61
                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                      TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                           NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE: Concu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: CARELLA, BYRNE, BAIN, GILI
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
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                                                       MEPPGDWGPPPWRSTPRTDVLRLVLYLTFLGAPCYAPALPSCKEDEYPVGSECCPKCSPG 60
YRVKEACGELTGTVCEPCPPGTYIAHLNGLSKCLQCQMCDPAMGLRASRNCSRTENAVCG
             YRVKEACGELTGTVCEPCPPGTYIAHLNGLSKCLQCQMCDPAMGLRASRNCSRTENAVCG 120
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                                                                                                                     283;
                                                                                                                     Conservative
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                                                                                                                  Score 1578; DB 1;
Pred. No. 3.6e-119;
; Mismatches 0;
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US-08-462-315-2

Sequence 2, Application US/08462315 GENERAL INFORMATION:

APPLICANT:

NI, ET AL.

Tumor Necrosis Factor Receptors

TITLE OF INVENTION: TU NUMBER OF SEQUENCES: 1 CORRESPONDENCE ADDRESS:

ADDRESSEE:

CARELLA, BYRNE, BAIN, GILFILLAN,

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PCT-US99-20180-13
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GENERAL INFORMATION:
APPLICANT: Millennium Biotherapeutics, Inc.
TITLE OF INVENTION: NOVEL MOLECULES OF THE H
TITLE OF INVENTION: PROTEIN FAMILY AND USES
FILE REFERENCE: 09404/079W01
CURRENT APPLICATION NUMBER: PCT/US99/20180
CURRENT FILING DATE: 1999-09-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                    Matches
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Best Local Similarity
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SOFTWARE: FastSEQ for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EARLIER APPLICATION NUMBER: US 09/342,767
EARLIER FILING DATE: 1999-66-29
EARLIER APPLICATION NUMBER: US 09/146,950
EARLIER FILING DATE: 1998-09-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 28
TYPE: PRT
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VQRKRQEAEGEATVIEALQAPPDVTTVAVEETIPSFTGRSPNH
                                                                                                                                                       CSPGHFCIVQDGDHCAACRAYATSSPGQRVQKGGTESQDTLCQNCPPGTFSPNGTLEECQ 180
                VQRKRQEAEGEATVIEALQAPPDVTTVAVEETIPSFTGRSPNH 283
                                                           HQTKCSWLVTKAGAGTSSSHWVWWFLSGSLVIVIVCSTVGLIICVKRRKPRGDVVKVIVS 240
                                                                                          HQTKCSWLVTKAGAGTSSSHWVWWFLSGSLVIVIVCSTVGLIICVKRRKPRGDVVKVIVS 240
                                                                                                                          CSPGHFCIVQDGDHCAACRAYATSSPGQRVQKGGTESQDTLCQNCPPGTFSPNGTLEECQ
                                                                                                                                                                                       YRVKEACGELTGTVCEPCPPGTYIAHLNGLSKCLQCQMCDPAMGLRASRNCSRTENAVCG
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                                                                                                                                                                                                                                                                                                                  283;
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                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                 100.0%;
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Pred. No. 3.
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283
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CITY: ROSELAND STATE: NEW JERSEY

ADDRESSEE: CECCHI, STEWART & OLSTEIN STREET: 6 BECKER FARM ROAD

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                                                                                                                          Sequence 2, Application US/08462962
GENERAL INFORMATION:
APPLICANT: NI, ET AL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
                                                                             CORRESPONDENCE ADDRESS:
                                                                                              TITLE OF INVENTION: Tumor Necrosis Factor Receptors NUMBER OF SEQUENCES: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 283 AMINO ACIDS
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 201-994-1700
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FILING DATE: June 5, 1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
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MEDIUM TYPE: 3.5 INCH DISKETTE
                                                                                                                                                                                                                                                                                                           181
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                            STREET:
                                               ADDRESSEE:
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Local Similarity 100.0%;
ses 283; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: PCT/US95/05058 FILING DATE: 27 APR 95
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                ROSELAND
NEW JERSEY
                            E: CARELLA, BYRNE, BAIN, GILI
E: CECCHI, STEWART & OLSTEIN
6 BECKER FARM ROAD
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Pred. No. 3.6e-119;
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                                                            GILFILLAN
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US-08-464-595-2
                                                                                                                                                                                                       Sequence 2, Application US/08464595
GENERAL INFORMATION:
APPLICANT: JIAN NI, REINER GENTZ AND CRAIG ROSEN
TITLE OF INVENTION: Tumor Necrosis Factor Receptors
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Best Local Similarity
Matches 283; Conserv
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INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 283 AMINO ACIDS
TYPE: AMINO ACID
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
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MEDIUM TYPE: 3.5 INC
COMPUTER: IBM PS/2
                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 27 APR 95
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 HQTKCSWLVTKAGAGTSSSHWVWWFLSGSLVIVIVCSTVGLIICVKRRKPRGDVVKVIVS 240
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                                                                                            STREET: 6 BECKI
CITY: ROSELAND
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                                     ZIP: 07068
                                                       COUNTRY:
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                                                                                                                                  ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/462,962. FILING DATE: June 5, 1995
                                                                                                                                                    ADDRESSEE:
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                                                                           NEW JERSEY
                                                                                                              6 BECKER FARM ROAD
                                                         USA
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                                                                                                                                  CECCHI,
                                                                                                                                CARELLA, BYRNE, BAIN, GILFILLAN CECCHI, STEWART & OLSTEIN
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Gaps

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APPLICATION NUMBER: PCT/US95/05058
FILING DATE: April 27, 1995
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 32,073
REFERENCE/DOCKET NUMBER: 325800-375
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700

325800-375

PRIOR APPLICATION DATA:

CLASSIFICATION:

SOFTWARE: WORD PERFECT CURRENT APPLICATION DATA:

SYSTEM: MS-DOS WORD PERFECT 5.1

COMPUTER: IBM PS/ OPERATING SYSTEM:

APPLICATION NUMBER: US/08, FILING DATE: June 5, 1995

US/08/464,595

TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:

TYPE: AMINO ACID

LENGTH:

283 AMINO ACIDS

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Best Local
                                  PRIOR APPLICATION NUMBER: US 08/464,595
PRIOR FILING DATE: 1995-06-05
PRIOR APPLICATION NUMBER: US 08/462,962
PRIOR FILING DATE: 1995-06-05
PRIOR APPLICATION NUMBER: US 08/462,315
PRIOR FILING DATE: 1995-06-05
PRIOR FILING DATE: 1995-06-05
PRIOR FILING DATE: 1995-04-27
                                                                                                                                                                                          TITLE OF INVENTION: Human Tumor Necrosis FILE REFERENCE: 1488.0770004 CURRENT APPLICATION NUMBER: US/08/741,095B CURRENT FILING DATE: 1996-10-30
SOFTWARE:
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                        NUMBER OF SEQ ID NOS:
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TOPOLOGY: LI
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                                                                                                                                                                                                                                                                       Rosen, Craig
Gentz, Reiner
    PatentIn version 3.0
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Conservative

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Gaps

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; LENGTH: 283 amino
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-987-902-1
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Query Match
Best Local Similarity
Matches 283; Conserv
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GENERAL INFORMATION:
APPLICANT: Avi J. Ashkenazi and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 283; Conserv
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LENGTH: 283
                                                                                                                                                                              TELEFAX: 650/952-9881 INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION: NAME: Marschang, Diane L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Avi J. Ashkenazi and Scot A. Marsters TITLE OF INVENTION: HVEM Polypeptides and Uses TO NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                 NAME: Marschang, Diane L. REGISTRATION NUMBER: 35,600
                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 YRVKEACGELTGTVCEPCPPGTYIAHLNGLSKCLQCQMCDPAMGLRASRNCSRTENAVCG 120
                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/987,902
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 100.0%; Score 1578; DB 13; 100.0%; Pred. No. 3.6e-119; tive 0; Mismatches 0;
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                                   Length 283;
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US-09-342-767-13
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US-09-342-767-13
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LENGTH: 283
TYPE: PRT
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Best Local :
                                                                                                                                                                                                                                                                                                 Matches
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TITLE OF INVENTION: NOVEL MOLECULES OF THE
TITLE OF INVENTION: HERPESVIRUS-ENTRY-MEDIATOR-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
FILE REFERENCE: MBIO98-061CP1
CURRENT APPLICATION NUMBER: US/09/342,767
CURRENT FILING DATE: 1999-06-29
EARLIER APPLICATION NUMBER: US 09/146,950
EARLIER FILING DATE: 1998-09-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: SIGNAL LOCATION: (1)...
                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
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241
                          241 VQRKRQEAEGEATVIEALQAPPDVTTVAVEETIPSFTGRSPNH 283
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                                                                                                                                CSPGHFCIVQDGDHCAACRAYATSSPGQRVQKGGTESQDTLCQNCPPGTFSPNGTLEECQ 180
                                                                       HQTKCSWLVTKAGAGTSSSSHWVWWELSGSLVIVIVCSTVGLIICVKRRKPRGDVVKVIVS
                                                                                                                                                                             YRVKEACGELTGTVCEPCPPGTYIAHLNGLSKCLQCQMCDPAMGLRASRNCSRTENAVCG 120
                                                                                                                                                                                           YRVKEACGELTGTVCEPCPPGTYIAHLNGLSKCLQCQMCDPAMGLRASRNCSRTENAVCG 120
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VQRKRQEAEGEATVIEALQAPPDVTTVAVEETIPSFTGRSPNH 283
                                                         HQTKCSWLVTKAGAGTSSSHWVWWFLSGSLVIVIVCSTVGLIICVKRRKPRGDVVKVIVS
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                                                                                                                                                                                                                                                                                               100.0%; Score 1578; DB 17; ilarity 100.0%; Pred. No. 3.6e-119; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                           DB 17;
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Best Local
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SEQUENCE CHARACTERISTICS:
                                                                                                    241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: Amino Acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: South San
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Sequence 26, Application US/09533262 GENERAL INFORMATION:
APPLICANT: Ni, Jian
APPLICANT: Rosen, Craig A.
APPLICANT: Gentz, Reiner L.
TITLE OF INVENTION: Human Tumor Nec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/09480284
GENERAL INFORMATION:
APPLICANT: Avi J. Ashkenazi and Scot A.
                                                                                                                                                                                                                                                      241 VQRKRQEAEGEATVIEALQAPPDVTTVAVEETIPSFTGRSPNH
                                                                                                                                                                                                                                                                                                                                                                                                             121 CSPGHFCTVQDGDHCAACRAYATSSPGQRVQKGGTESQDTLCQNCPPGTFSPNGTLEECQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: P1068R1 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 08/987,902
FILING DATE: 10-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: MATSCHANG, DIANG L.
REGISTRATION NUMBER: 35,600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/480,284 FILING DATE: 10-Jan-2000 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 mb floppy
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE DESCRIPTION: SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: HVEM Polypeptides
                                                                                                                                                                                                                                                                                                                    HQTKCSWLVTKAGAGTSSSHWVWWFLSGSLVIVIVCSTVGLIICVKRRKPRGDVVKVIVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CSPGHFCIVQDGDHCAACRAYATSSPGQRVQKGGTESQDTLCQNCPPGTFSPNGTLEECQ
                                                                                                                                                                                                                               VQRKRQEAEGEATVIEALQAPPDVTTVAVEETIPSFTGRSPNH
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TELEFAX: 650/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 283 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 1578; DB 18; 100.0%; Pred. No. 3.6e-119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genentech,
  Tumor Necrosis Factor Receptor-Like
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and Uses Thereof
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; SOFTWARE: PatentIn Ver. 2
; SEQ ID NO 26
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-533-262-26
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Best Local S
Matches 283
                                                                                                                                                                                                                                                                                                               Sequence 46, Applica GENERAL INFORMATION:
FILE OF ANTICATION NUMBER: US/09/882,636
CURRENT APPLICATION NUMBER: US/09/882,636
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: 60/113,296
PRIOR FILING DATE: December 22, 1998
PRIOR FILING DATE: December 32, 1998
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EARLIER
                                                                                                                         APPLICANT: WOOD, WILLIAM, I.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF TUMOR FILE REFERENCE: P2509R1C1
                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                           APPLICANT: Botstein, David
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RAPPLICATION NUMBER: US 60/125,683

ER FILING DATE: 1999-03-22

ER APPLICATION NUMBER: US 08/741,095

ER FILING DATE: 1996-10-30

ER APPLICATION NUMBER: US 08/464,595

ER FILING DATE: 1995-06-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YRVKEACGELTGTVCEPCPPGTYIAHLNGLSKCLQCQMCDPAMGLRASRNCSRTENAVCG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HQTKCSWLVTKAGAGTSSSHWVWWFLSGSLVIVIVCSTVGLIICVKRRKPRGDVVKVIVS 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CSPGHFCIVQDGDHCAACRAYATSSPGQRVQKGGTESQDTLCQNCPPGTFSPNGTLEECQ 180
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APPLICATION NUMBER: US 08/462,315
FILING DATE: 1995-06-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 60/135,169
FILING DATE: 1999-05-20
APPLICATION NUMBER: US 60/126,522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 08/462,962
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 2000-03-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                             Goddard, Audrey
Gurney, Austin L.
Hillan, Kenneth
                                                                                                                                                                                                                                                                                                                                         Application US/09882636
                                                                                                                                                                                     Roy, Margaret, Ann
                                                                                                                                                                                                         Lawrence, David, A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OR FILING DATE: May 30, 2000
OR APPLICATION NUMBER: PCT/US00/13705
OR FILING DATE: May 17, 2000
OR APPLICATION NUMBER: PCT/US00/08439
OR FILING DATE: March 30, 2000
OR APPLICATION NUMBER: PCT/US00/05841
OR APPLICATION NUMBER: PCT/US00/05841
OR FILING DATE: March 2, 2000
OR APPLICATION NUMBER: PCT/US00/05004
OR FILING DATE: February 24, 2000
OR FILING DATE: February 24, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OR FILING DATE: January 5, 1998
OR APPLICATION NUMBER: 60/069,873
OR FILING DATE: December 17, 1997
OR APPLICATION NUMBER: 60/069,702
OR FILING DATE: December 16, 1997
OR APPLICATION NUMBER: 60/069,694
OR FILING DATE: December 16, 1997
OR APPLICATION NUMBER: 60/069,696
OR FILING DATE: December 16, 1997
OR APPLICATION NUMBER: 60/060,702
OR APPLICATION NUMBER: 60/066,772
OR APPLICATION NUMBER: 60/063,705
OR APPLICATION NUMBER: 60/032,705
                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: February 18, 2000
APPLICATION NUMBER: PCT/US00/04342
FILING DATE: February 18, 2000
APPLICATION NUMBER: 09/480,284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: February 22, 2000
APPLICATION NUMBER: PCT/US00/04341
FILING DATE: February 18, 2000
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APPLICATION NUMBER: 09/664,610
FILING DATE: September 18, 2000
APPLICATION NUMBER: 09/665,350
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APPLICATION NUMBER: 60/083,500
FILING DATE: April 29, 1998
                                                                                                                     FILING DATE: APPLICATION
                                                                                                                                                                                                                                                                       APPLICATION FILING DATE:
                                                                                                                                                                                                                                                                                                                                       FILING DATE: APPLICATION
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FILING DATE: May 30, 2000
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APPLICATION NUMBER: 60/074,086
FILING DATE: February 9, 1998
APPLICATION NUMBER: 60/070,440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: December 16, 1998
APPLICATION NUMBER: 60/107,783
FILING DATE: NOvember 10, 1998
APPLICATION NUMBER: 60/088,742
                                                       FILING DATE:
                                                                           APPLICATION
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FILING DATE: August 23, 2000
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FILING DATE: April 23, 1998
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                                 NUMBER: PCT/US99/
: September 1, 199
NUMBER: 09/380,13
                                                                                                                                                                                                                                                                                                                                                                               : January 10, 2000
NUMBER: PCT/US99/30095
                                                                                                                : October 18, 1999
NUMBER: PCT/US99/21090
                                                                                                                                                               : November 30, 1999
NUMBER: 09/403,297
                                                                                                                                                                                                                                                                                                                                     NUMBER: PCT/US99/28565
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RESULT 13
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; Sequence 60, Application US/09886342
; GENERAL INFORMATION:
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SEQ ID NO 46
LENGTH: 283
TYPE: PRT
ORGANISM: Homo SIS-09-882-636-46
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IOR APPLICATION NUMBER: PCT/US99/1222
IOR FILING DATE: June 2, 1999
IOR APPLICATION NUMBER: PCT/US99/08847
IOR FILING DATE: April 23, 1999
IOR APPLICATION NUMBER: 09/284, 404
IOR FILING DATE: April 23, 1999
IOR APPLICATION NUMBER: 09/284, 291
IOR APPLICATION NUMBER: 09/284, 291
IOR APPLICATION NUMBER: 09/284, 291
IOR APPLICATION NUMBER: PCT/US99/05028
IOR FILING DATE: MATCH 8, 1999
IOR FILING DATE: 
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OR APPLICATION NUMBER: 09/254,311
OR FILING DATE: MArch 3, 1999
OR APPLICATION NUMBER: PCT/US99/00106
OR FILING DATE: January 5, 1999
OR APPLICATION NUMBER: 09/218,517
OR APPLICATION NUMBER: 09/218,517
OR FILING DATE: December 22, 1998
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APPLICATION NUMBER: 09/065,2/5
FILING DATE: APPLI 23, 1998
{ APPLICATION NUMBER: 08/987,902
{ APPLICATION December 10, 1997
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FILING DATE: December 16
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APPLICATION NUMBER:
FILING DATE: August
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                                                                                                                                                                                                                                                                                                                            HQTKCSWLVTKAGAGTSSSHWVWWFLSGSLVIVIVCSTVGLIICVKRRKPRGDVVKVIVS 240
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Pred. No. 3.6e-119;
; Mismatches 0;
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PRIOR APPLICATION NUMBER: 60/131,445
PRIOR FILING DATE: April 28, 1999
PRIOR APPLICATION NUMBER: 60/134,287
PRIOR FILING DATE: May 14, 1999
PRIOR APPLICATION NUMBER: 60/144,758
PRIOR APPLICATION NUMBER: 60/145,698
PRIOR APPLICATION NUMBER: 60/145,698
PRIOR FILING DATE: July 26, 1999
PRIOR FILING DATE: July 26, 1999
PRIOR APPLICATION NUMBER: 08/934,494
PRIOR FILING DATE: September 19, 1997
PRIOR APPLICATION NUMBER: 08/933,821
PRIOR FILING DATE: September 19, 1997
PRIOR APPLICATION NUMBER: 08/933,821
PRIOR FILING DATE: September 19, 1997
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PRIOR FILING DATE: December 12, 1996
PRIOR APPLICATION NUMBER: 60/059,115
PRIOR APPLICATION NUMBER: 60/059,118
PRIOR APPLICATION NUMBER: 60/059,184
PRIOR FILING DATE: September 17, 1997
PRIOR APPLICATION NUMBER: 60/059,352
PRIOR FILING DATE: September 19, 1997
PRIOR APPLICATION NUMBER: 60/059,588
PRIOR FILING DATE: September 19, 1997
PRIOR APPLICATION NUMBER: 60/059,588
PRIOR FILING DATE: September 19, 1997
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TITLE OF INVENTION: METHODS AND COMPOSITIONS
TITLE OF INVENTION: CELL GROWTH
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CURRENT FILING DATE: 2001-06-19
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OR FILING DATE: September 17, 1998
OR APPLICATION NUMBER: 60/113,296
OR FILING DATE: December 22, 1998
OR APPLICATION NUMBER: 60/109,304
OR FILING DATE: November 20, 1998
OR APPLICATION NUMBER: 60/130,232
OR APPLICATION NUMBER: 60/130,232
OR FILING DATE: April 21, 1999
OR FILING DATE: April 21, 1999
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                                                                                                                                                  APPLICATION NUMBER: PCT/US97
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APPLICATION NUMBER: 60/131, value of the control 
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                                     APPLICATION NUMBER: 08/987,
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Pitti, Robert, M.
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OR APPLICATION NUMBER: 09/333,077
OR FILING DATE: June 14, 1999
OR APPLICATION NUMBER: 09/380,138
OR FILING DATE: August 25, 1999
OR APPLICATION NUMBER: 09/380,139
OR FILING DATE: August 25, 1999
OR APPLICATION NUMBER: 07/05/05/21090
OR APPLICATION NUMBER: 07/05/05/21090
OR FILING DATE: September 15, 1999
OR FILING DATE: September 15, 1999
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R FILING DATE: MUMBER: 09/284,291
R FILING DATE: April 12, 1999
R FILING DATE: June 14, 1999
R FILING DATE: June 14, 1999
R APPLICATION NUMBER: 09/332,929
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FILING DATE:
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APPLICATION NUMBER: 09/403,296
FILING DATE: October 18, 1999
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                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: PCT/US99/21547 FILING DATE: September 15, 1999
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FILING DATE: October 9, 1998
APPLICATION NUMBER: PCT/US98/24855
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FILING DATE: October 9, 1998
APPLICATION NUMBER: 05/169,1098
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FILING DATE: September 14, 1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 09/254,460 FILING DATE: March 9, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/US99/00106 FILING DATE: January 5, 1999
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                      January 5, 2000
| NUMBER: PCT/US00/00277
| January 6, 2000
| NUMBER: 09/480,284
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; NUMBER OF SEQ ID NOS: 79
; SEQ ID NO 60
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-886-342-60
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PRIOR FILING DATE: March 1
NUMBER OF SEQ ID NOS: 79
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PRIOR APPLICATION NUMBER: 09/690,169
PRIOR FILING DATE: October 16, 2000
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PRIOR PELICATION NUMBER: PCT/US00/13705
PRIOR FILING DATE: May 17, 2000
PRIOR APPLICATION NUMBER: PCT/US00/14042
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: PCT/US00/07377 PRIOR FILING DATE: March 20, 2000
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PRIOR APPLICATION NUMBER: PCT/US00/04414
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OR FILING DATE: May 22, 2000
OR APPLICATION NUMBER: PCT/US00/15264
OR FILING DATE: June 2, 2000
OR APPLICATION NUMBER: 09/64,610
FILING DATE: September 18, 2000
FILING DATE: September 18, 2000
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APPLICATION NUMBER: PCT/US00/05841
FILING DATE: March 2, 2000
APPLICATION NUMBER: PCT/US00/06884
FILING DATE: March 15, 2000
FILING DATE: March 15, 2000
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APPLICATION NUMBER: PCT/US00/32678
FILING DATE: December 1, 2000
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                  VQRKRQEAEGEATVIEALQAPPDVTTVAVEETIPSFTGRSPNH
                                                                         HQTKCSWLVTKAGAGTSSSHWVWWFLSGSLVIVIVCSTVGLIICVKRRKPRGDVVKVIVS
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RESULT 14
US-09-35-727-31
; Sequence 31, Application US/09935727
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.

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RESULT 15
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; LENGTH: 283
; TYPE: PRT
; ORCANISM: Homo sapiens
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CURRENT FILING DATE: 2001-08-24
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FILING DATE: 1999-08-02
APPLICATION NUMBER: 60/131,964
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FILING DATE: 1998-01-13
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APPLICATION NUMBER: 60/121,774
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                                                                                                                   Application PC/TUS9618540
Wing of Prussia, PA 1940
United States of America
                        Rockville, MD 20850
United States of America
709 Swedeland Road
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                                                                    9410 Key West Avenue
                                                                                     Human Genome Sciences,
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; MOLECULE TYPE: protein PCT-US96-18540-2
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CLASSIFICATION:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Goldstein, Jorge A.
NAME: Goldstein, Jorge A.
14
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REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICANT: Lyn, Sally Doreen Patricia
APPLICANT: Hurle, Mark Robert
TITLE OF INVENTION: Human Tumor Necro
TITLE OF INVENTION: Receptor-Like 2
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ZIP: 20005-3934
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VQRKRQEAEGEATVIEALQAPPDVTTVAVEETIPSFTGRSPNH
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1100 New York Ave, Suite
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Suite 600
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1: /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep:*

2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*

3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*

4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*

5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*

6: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*

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US-09-896-096A-1
US-09-840-795-2
US-09-840-795-2
US-09-840-795-9
US-09-840-795-9
US-09-879-845-7
US-09-879-845-1
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US-09-877-650-2
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-924-231-2
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US-09-924-231-2
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SEQ ID NO 2
LENGTH: 283
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Best Local Similarity
Matches 283; Conserv
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Result No.

45	44	43	42	41	40	39	38	37	36	35	34	ω W	32	31	30	29	28	27
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Þ	Sequence 22, Appl	Sequence 11, Appl		Sequence 15, Appl	21		9	Sequence 18, Appl	Sequence 15, Appl	Sequence 4, Appli	Sequence 8, Appli	Sequence 2, Appli	Sequence 4, Appli	Sequence 6, Appli	Sequence 64, Appl	Sequence 64, Appl	Sequence 64, Appl	Sequence 64, Appl

ALIGNMENTS

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Sequence 2, Application US/09924231 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 09/33,279
PRIOR FILING DATE: 1999-06-15
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Date: Date: 1999-06-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: SPEAR, Patricia G.
APPLICANT: MONTGOMERY, Rebecca I.
TITLE OF INVENTION: HERPES VIRUS ENTRY RECEPTOR PROTEIN
FILE REFERENCE: 0290-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/924,231
CURRENT FILING DATE: 2001-08-08
181 HQTKCSWLVTKAGAGTSSSHWVWWFLSGSLVIVIVCSTVGLIICVKRRKPRGDVVKVIVS
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GENERAL INFORMATION:

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; SEQ ID NO 2
; LENGTH: 277
; TYPE: PRT
; ORCANISM: Homo sapiens
US-09-855-528-2
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US-09-855-528-2
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                                                         Matches
                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/09855528 GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 1999-06-15
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: NOELLE, RANDOLPH J.

APPLICANT: BURNS, CHRISTOPHER M.

TITLE OF INVENTION: USE OF ANTI-GP-39 ANTIBODIES FOR TREATMENT AND/OR

TITLE OF INVENTION: REVERSAL OF LUPUS AND LUPUS ASSOCIATED KIDNEY DISEASE

FILE REFERENCE: 037003-0280622
                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/855,528
CURRENT FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: 09/054,488
PRIOR FILING DATE: 1998-04-03
                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 1992-02-14 NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 08/742,480 PRIOR FILING DATE: 1996-11-01 PRIOR APPLICATION NUMBER: 08/338,975 PRIOR FILING DATE: 1994-11-14
                                                                                                                                                                                                                                                SOFTWARE: Patentin Ver.
                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 07/835,799
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CURRENT FILING DATE: 2001-08-08
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TITLE OF INVENTION: HERPES VIRUS ENTRY RECEPTOR PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: SPEAR, Patricia G. APPLICANT: MONTGOMERY, Rebec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 419
TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 CSPGHFCIVQDGDHCAACRAYATSSPGQRVQKGGTESQDTLCQNCPPGTFSPNGTLEECQ 180
HQTKC 185
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                                                           Conservative
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                                                                            17.0%;
26.1%;
                                                           50;
                                                     Score 267.5; DB 5;
Pred. No. 5.5e-16;
50; Mismatches 116;
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                                                         Indels
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Best Local Similarity
Matches 59; Conserv
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                                          APPLICANT: Murphy, Erin E.

APPLICANT: Mattson, Jeanine D.

APPLICANT: Bates, Elizabeth Esther Mary

APPLICANT: Gorman, Daniel M.

APPLICANT: Lebecque, Serge J.E.

TITLE OF INVENTION: Mammalian Genes; Related Reagents

FILE REFERENCE: SF0818K
  CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/852,455
CURRENT FILING DATE: 2001-05-09
PRIOR APPLICATION NUMBER: 60/202,912
                      CURRENT APPLICATION NUMBER: US/09/840,795
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NUMBER OF SEQ ID NOS: 81
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APPLICANT: PRENDERGAST, JOHN
TITLE OF INVENTION: METHODS OF IDENTIFYING THE ACTIVITY OF GENE PRODUCTS
FILE REFERENCE: 2598-4004US1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: BLUME, ARTHUR J. APPLICANT: GOLDSTEIN, NEIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       135 CAACRAYATSSPGQRVQKGGTESQDTLCQNCPPGTFS-PNGTLEECQHQTKCSW--LVTK 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               226 AP--HPKQEPQEINFPDDLPGSKTAAPVQETL 255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92 KCLQCQMCDPAMGLRASRN-----CSRTENAVCGCSPGHFCIVQDGDHCAACRAYATSS 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 YAPEPGSTCRLREYYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDSCEDSTYTQLWNWVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35 YAPALPS-CKEDEY--PVGSECCPKCSPGYRVKEACGELTGTVCEPCPPGTYIAHLNGLS 91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MVRLPLQCVLWG--CLLTAVHPEPPTACREKQYLINSQCCSLCQPGQKLVSDCTEFTETE 58
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2001-04-23
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RESULT 7
US-09-896-096A-17
Sequence 17, Application US/09896096A
GENERAL INFORMATION:
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; TYPE: PRT
; ORGANISM: Homo sapien
US-09-579-845-10
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; ORGANISM: primate
US-09-840-795-10
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Best Local Similarity
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LENGTH: 225
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CURRENT FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/150,688
PRIOR FILING DATE: 1999-05-28
NUMBER OF SEQ ID NOS: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Burstein, Haim
APPLICANT: Stepan, Anthony M.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TITLE OF INVENTION: THE LEVEL OF TUMOR NECROSIS
TITLE OF INVENTION: DISORDERS
FILE REFERENCE: 226272004420
APPLICANT: ASHKENAZI, AVI J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.0
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                                                                                                                                                                        146 PGQRVQKGGTESQDTLCQNCPPGTFS-PNGTLEECQHQTKCSWLVTKAGAG-----TSSS 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             145 PGFGVARPGTETSDVVCKPCAPGTESNTTSSTDICRPHQICNVVAIPGNASMDAVCTSTS 204
                                                                                                                                                145 PGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICRPHQICNVVAIPGNASMDAVCTSTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       146 PGQRVQKGGTESQDTLCQNCPPGTFS-PNGTLEECQHQTKCSWLVTKAGAG-----TSSS 199
                                                                                                                                                                                                                                                                       92 KCLQCQMCDPAMGLRASRN-----CSRTENAVCGCSPGHFCIVQDGDHCAACRAYATSS 145
                                                                                                                                                                                                                                                                                                                          32
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Local Similarity 32.8%;
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                                                                                                                                                                                                                               ECLSC-----GSRCSSDQVETQACTREQNRICTCRPGWYCALSKQEGCRLCAPLRKCR 144
                                                                                                                                                                                                                                                                                                                    YAPEPGSTCRLREYYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDSCEDSTYTQLWNWVP 91
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                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                            16.4%; Score 259; DB 5; 32.8%; Pred. No. 2.8e-15;
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Pred. No. 2.4e-15;
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LENGTH: 518
TYPE: PRT
ORGANISM: Homo sapien
US-09-579-845-1
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Query Match 16.4
Best Local Similarity 32.8
Matches 59; Conservative
                                                                                                                                                                                           SOFTWARE: FastSEQ
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/09579845 GENERAL INFORMATION:
                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/150,688
PRIOR FILING DATE: 1999-05-28
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PRIOR SOFTWARE:
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Best Local (
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                                                                                                                                                                                                                                                                                                APPLICANT: Burstein, Haim
APPLICANT: Stepan, Anthony M.
APPLICANT: Stepan, Anthony M.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TITLE OF INVENTION: THE LEVEL OF TUMOR NECROSIS
TITLE OF INVENTION: DISORDERS
FILE REFERENCE: 226272004420
CURRENT APPLICATION NUMBER: US/09/579,845
CURRENT FILING DATE: 2000-05-26
CURRENT FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: DCR3 POlypeptide, A THER ETILE REFERENCE: P1134R2 REVISED CURRENT SEPLICATION NUMBER: US/09/896,096A CURRENT FILING DATE: 2001-06-28 PRIOR APPLICATION NUMBER: US 09/157,289 PRIOR FILING DATE: 1998-09-18 PRIOR APPLICATION NUMBER: US 60/059,288 PRIOR APPLICATION NUMBER: US 60/059,288 PRIOR ETILING DATE: 1997-09-18
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TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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Local Similarity 32.8%; Pred. No. 4.9e-15;
hes 59; Conservative 23; Mismatches 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32 YAPEPGSTCRLREYYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDSCEDSTYTQLWNWVP 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICRPHQICNVVAIPGNASRDAVCTSTS 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ECLSC-----GSRCSSDQVETQACTREQNRICTCRPGWYCALSKQEGCRLCAPLRKCR 144
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WOOD, WILLIAM I.
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LAWRENCE, DAVID A.
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GURNEY, AUSTIN L.
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16.4%; Score 259; DB 5; I 32.8%; Pred. No. 5.5e-15; tive 23; Mismatches 76;
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35 YAPALPS-CKEDEY--PVGSECCPKCSPGYRVKEACGELTGTVCEPCPPGTYIAHLNGLS 91

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Best Local Similarity 32.8
Matches 59; Conservative
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APPLICANT: Stepan, Anthony M.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TITLE OF INVENTION: THE LEVEL OF TUMOR NECROSIS
TITLE OF INVENTION: DISORDERS
                                                                    TITLE OF INVENTION: DCR3 POlypeptide, A TNFR Homolog FILE REFERENCE: P1134R2 REVISED CURRENT APPLICATION NUMBER: US/09/896,096A CURRENT FILING DATE: 2001-06-28
                                                                                                                                                                                                                                     APPLICANT: ASHKENAZI, AVI J
APPLICANT: BOTSTEIN, DAVID
APPLICANT: DODGE, KELLY H.
APPLICANT: GURNEY, AUSTIN L.
APPLICANT: KIM, KYUNG JIN
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PRIOR FILING DATE: 1999-05-28
NUMBER OF SEQ ID NOS: 20
PRIOR FILING DATE:
                 PRIOR APPLICATION NUMBER: US 60/059,288
                                  PRIOR APPLICATION NUMBER: US 09/157,289 PRIOR FILING DATE: 1998-09-18
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CURRENT APPLICATION NUMBER: US/09/579,845
CURRENT FILING DATE: 2000-05-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YAPEPGSTCRLREYYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDSCEDSTYTQLWNWVP 120
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                                                                                                                                                                                                                                                                                                                                                     Application US/09896096A
                                                                                                                                               TUMAS, DANIEL B WOOD, WILLIAM I.
                                                                                                                                                                                   PITTI, ROBERT ROY, MARGARET A
                                                                                                                                                                                                                       LAWRENCE,
                                                                                                                                                                                                                     DAVID A.
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; NAME/KEY: misc_feature
; LCCATION: (79)
; OTHER INFORMATION: Xaa at residue 79
US-09-840-795-2
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; LEWOTH: 3000
; TYPE: PRT
; ORCANISM: Homo sapiens
US-09-896-096A-1
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LENGTH: 300
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APPLICANT: Murphy, Erin E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: SF0818K
CURRENT APPLICATION NUMBER: US/09/840,795
CURRENT FILING DATE: 2001-04-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Mammalian Genes; Related Reagents
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: primate FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
126 FCIVQDGDHCAACRAYATSSPGQRVQKGGTESQDTLCQNCPPGTFS-PNGTLEECQHQTK 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             175 TALGLALNVPGSSSH 189
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                                                                                                                                                                                                                                                        Local Similarity
nes 69; Conserv
                                                                    64 RDSPMTCGPCPPRHYTQFWNYLERCRXCYVLC----GEREEEARACHATHNRACRCRTGF 119
                                                                                                                                                                                                           16 PRTDVLRLVLYLTFLGAPCYAPALPSCKE-DEYP-----VGSE-CCPKCSPGYRVKEACG 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 RDSPTTCGPCPPRHYTQFWNYLER----CRYCNVLCGEREEEARACHATHNRACRCRTGFF 120
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                                                                                                                 ELTGTVCEPCPPGTYIAHLNGLSKCLQCQ-MCDPAMGLR--ASRNCSRTENAVCGCSPGH 125
                                                                                                                                                              PGLSLLCLVLALPAL - - - LPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQRPCR 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A-----HAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNC
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Bates, Elizabeth Esther Mary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gorman, Daniel M.
                                                                                                                                                                                                                                                        Conservative
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35.2%;
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                                                                                                                                                                                                                                                     ; Score 239; DB 5;
; Pred. No. 1.7e-13;
15; Mismatches 88
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                                                                                                                                                                                                                                                                                                  Length 300;
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RESULT 13
US-09-579-845-14
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US-10-003-211-1
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                                                                                                  GENERAL INFORMATION.

APPLICANT: Burstein, Haim
APPLICANT: Stepan, Anthony M.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR LOWERING
TITLE OF INVENTION: THE LEVEL OF TUMOR NECROSIS FACTOR (7

TITLE OF INVENTION: DISORDERS
FILE REFERENCE: 226272004420

CURRENT APPLICATION NUMBER: US/09/579,845

TURNERM FILING DATE: 2000-05-26
                SEQ ID NO 14
LENGTH: 487
                                                                                                                                                                                                                                                                                             Sequence 14, Application US/09579845 GENERAL INFORMATION:
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Best Local
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                                                                                       CURRENT FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/150,688
PRIOR FILING DATE: 1999-05-28
                                                      NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: PCT/US97/19436
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/029,060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Browning, et al.
TITLE OF INVENTION: Soluble Lymphotoxin Beta Receptor and
TITLE OF INVENTION: Anti-Lymphotoxin Receptor and Ligand
TITLE OF INVENTION: Therapeutic Agents for the Treatment
TITLE OF INVENTION: Diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 1996-10-25
NUMBER OF SEQ ID NOS: 1
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/003,211 CURRENT FILING DATE: 2001-10-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Biogen, Inc. APPLICANT: Browning, 6
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TYPE: PRT
TYPE: PRT
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56; Conserv
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                                                      20
Windows Version 4.0
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Pred. No. 6.2e-13;
Mismatches 66;
                                                                                                                                                                                                                FACTOR (TNF) IN TNF-ASSOCIATED
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; TYPE: PRT
; ORGANISM: Rattus rattus
US-09-579-845-7
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                                                                                                                                                                                                                                                                                                                                  Query Match 13.8
Best Local Similarity 25.4
Matches 60; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 20
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7, Application US/09579845 GENERAL INFORMATION:
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: 226272004420
CURRENT APPLICATION NUMBER: US/09/579,845
CURRENT FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/150,688
PRIOR FILING DATE: 1999-05-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Stepan, Anthony M.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR LOWERING
TITLE OF INVENTION: THE LEVEL OF TUMOR NECROSIS FACTOR (TNF)
TITLE OF INVENTION: DISORDERS
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  216 IYVSQPEP--
                                                                                                                                                                   112 TKKQNRVCACNADSYCALKLHSGNCRQCMKLSKCGPGFGVARSRTSNGNVICSACAPGTF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            112 SRTENAVCGCSPGHFCIVQ-DGDHCAACRAYATSSPGQRVQKGGTESQDTLCQNCPPGTF 170
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                                                                                                                                                                                                                                                       54 CCAKCPPGQYAKHFCNKTSDTVCADCAAGMFTQVWNHLHTCLSCSSSCSDDQ--VETHNC
                                                                                                                                                                                                                                                                                             53 CCPKCSPGYRVKEACGELTGTVCEPCPPGTYIAHLNGLSKCLQC-QMCDPAMGLRASRNC 111
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                                                                                                                     S-PNGTLEECQHQTKCSWLVTKAGAGTSSSHWVWWFLSGSLVIVIVC----STVGLI
                                                                                                                                                                                              SRTENAVCGCSPGHFCIVQ-DGDHCAACRAYATSSPGQRVQKGGTESQDTLCQNCPPGTF 170
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                                       ICVKRRKPRGDVVKVIVSVQRKRQEAEGEATVIEALQAPPDVTTVAVEETIPSFTG 278
                                                                                    SDTTSSTDVCRPHGICSILAIPGNASTDA---
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                                                                                                                                                                                                                                                                                                                                       13.8%; Score 217; DB 5; Length 258; 25.4%; Pred. No. 1.2e-11; Live 29; Mismatches 105; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----TRSQPMDQEPGPSQTPHIPVSLGSTPIIE--PSITGGVPR
-TRSQPMDQEPGPSQTPHIPVSLGSTPIIE--PSITG
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FILE REFERENCE: SF0818K
CURRENT APPLICATION NUMBER: US/09/840,795
CURRENT FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: 09/351,777
PRIOR FILING DATE: 1999-07-12
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 9
LENGTH: 227
TYPE: PAT
ORGANISM: rodent
US-09-840-795-9
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Search completed: January 24, 2002, 16:22:45 Job time: 90 sec
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US-09-840-795-9
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GENERAL INFORMATION:
APPLICANT: Muthy, Erin E.
APPLICANT: Mattson, Jeanine D.
APPLICANT: Bates, Elizabeth Esther Mary
APPLICANT: Gorman, Daniel M.
APPLICANT: Lebecque, Serge J.E.
TITLE DEFERENCE: GENOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match : 13.5%; Score 213.5; DB 5; Length 227; Best Local Similarity 28.5%; Pred. No. 2.1e-11; Matches 55; Conservative 20; Mismatches 101; Indels 17; Gaps
                                                                                                             188 SILAIPGNASTDA 200
                                                                                                                                                                                                 128 ALKTHSGSCRQCMRLSKCGPGFGVASSRAPNGNVLCKACAPGTFSDTTSSTDVCRPHRIC 187
                                                                                                                                                       186 SWLVTKAGAGTSS 198
                                                                                                                                                                                                                         128 IVQ-DGDHCAACRAYATSSPGQRVQKGGTESQDTLCQNCPPGTFS-PNGTLEECQHQTKC 185
                                                                                                                                                                                                                                                                                     11 VFELQLWATGHTVPAQVVLTPYKPEPGYECQISQEYYDRKAQMCCAKCPPGQYVKHFCNK 70
                                                                                                                                                                                                                                                                                                                                                                                                          20 VLRLVLYLTFLGAPCYAPALPSCKEDEY--PVGSE------CCPKCSPGYRVKEACGE 69
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Database
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Maximum Match 100%
Listing first 45 summaries
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ALIGNMENTS

B cell-associated surface molecule CD40, long splice form - mouse C;Species: Mus musculus (house mouse) C;Decies: Mas musculus (house mouse) C;Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 17-Nov-2000 C;Accession: A46476; A46515

R; Torres, R.M.; Clark,

RESULT A46476

A;Molecule type: nucleic acid
A;Residues: 1-287, LrV' <GRI2A;Cross references: GB:M83312; NID:g1553058; PIDN:AAB08705.1;
A;Cross references: GB:M83312; NID:g1553058; PIDN:AAB08705.1;
A;Cross references: GB:M83312; NID:g1553058; PIDN:AAB08705.1;
A;Experimental source: BALB/c, liver
A;Note: sequence extracted from NCBI backbone (NCBIP:120357)
C;Comment: For an alternative splice form, see PIR:A46515.
C;Comment: For an alternative splice form, see PIR:A46476.
C;Superfamily: CD27 antigen; NGF receptor repeat homology
C;Keywords: alternative splicing; transmembrane protein
F;105-144/Domain: NGF receptor repeat homology <NGF> A;Cross-references: GB:M83312; NID:g1553058
A;Note: sequence extracted from NCBI backbone (NCBIN:75206, NCBIP:75207)
A;Note: this translation is not annotated in GenBank entry MUSCD40A, release 113.
A;Note: this translation is not annotated in GenBank entry MUSCD40A, release 113.
R;Grimaldi, J.C.; Torres, R.; Kozak, C.A.; Chang, R.; Clark, E.A.; Howard, M.; Co
J. Immunol. 149, 3921-3926, 1992
A;Title: Genomic structure and chromosomal mapping of the murine CD40 gene.
A;Reference number: A46515; MUID:93094586
A;Recession: A46515
A;Status: preliminary; not compared with conceptual translation J. Immunol. 148, 620-626, 1992 A;Title: Differential increase of an alternatively polyadenylated mRNA species of mur A;Reference number: A46476; MUID:92105763 A;Accession: A46476 Q B Ş B Qy 밁 29 A; Molecule type: mRNA A; Residues: 1-305 < TOR> A;Status: preliminary Query Match Best Local S Matches 69 216 CSTVGLIIC-----VKR--RKPRGDVVKVIVSVQRKRQEAEGEATVIEALQAPPDVTT 266 101 161 LCONCPPGTFSPNGTL-EECQHQTKCS----WLVTKAGAGTSSSHWVWWFLSGSLVIVIV 215 25 41 SCKEDEYPVGSECCPKCSPGYRVKEACGELTGTVCEPCPPGTYIAHLNGLSKCLQCQMCD 100 PAMGLRASRNCSRTENAVCGCSPGHFCIVQDGDHCAACRAYATSSPGQRVQKGGTESQDT 160 TCSDKQYLHDGQCCDLCQPGSRLTSHCTALEKTQCHPCDSGEFSAQWNREIRCHQHRHCE 84 VCHPCPVGFFSNQSSLFEKCYPWTSCEDKNLEVLQK---GTSQTNVICGLKSRMRALLVI PNQGLRVKKEGTAESDTVCTCKEGQHCTSKD---CEACAQHTPCIPGFGVMEMATETTDT 69; Conservative 17.5%; 27.9%; 43; Score 276.5; DB 2; Length pred. No. 2.9e-13; Mismatches 106; Indels 305; PID:g1553059; GB:M94126 29; Gaps 198 141 Cockay .

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RESULT 3
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C;Superfamily: CD27 antigen; NGF receptor repeat homology
C;Keywords: B-cell; glycoprotein; phosphoprotein; surface antigen; transmembrane
F;1-20/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Title: Biochemical characteristics and partial amino acid sequence A; Reference number: A60771; MUID:89093941
A; Accession: A60771
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Homo sapiens (man)
C;Date: 03-Jun-1993 #sequence_revision 03-Feb-1994 #text_change
C;Accession: S04460; A60771
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;194-215/Domain: transmembrane #status predicted <TMM>F;216-277/Domain: intracellular #status predicted <CYT>F;153,180/Binding site: carbohydrate (Asn) (covalent) #:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;21-277/Product: B-cell activation protein CD40 #status experimental <MAT>F;21-193/Domain: extracellular #status predicted <EXT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: protein A; Residues: 21-50 <BRA>
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A; Title: A B-lymphocyte activation molecule related A; Reference number: S04460; MUID:89356608
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Gene: GDB:CD40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-277 < STA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Reference number: A; Accession: S04460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Experimental source: Burkitt lymphoma cell line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R; Stamenkovic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 71; Conser
                                                                                                                       226
                                                                                                                                                                                                        176
                                                                                                                                                                                                                                             192 AGAGTSSSHWVWWFLSGSLVIVIVCSTVGLIICVKRRKPRGDVVKVIVSVQRKRQEAEGE 251
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                                                                                                                                                                                                                                                                                                              CEPCPPGTYIAHLNGLSKCLQCQMCDPAMGLRASRNCSRTENAVCGCSPGHFCIVQDGDH 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                              MVRLPLQCVLWG--CLLTAVHPEPPTACREKQYLINSQCCSLCQPGQKLVSDCTEFTETE 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VLRLVLYLTFLGAPCYAPAL-----PSCKEDEYPVGSECCPKCSPGYRVKEACGELTGTV 74
                                                                                                                                                               ATVIEALQAPPDV---
                                                                                                                                                                                                        Q-AGTNKTDVVCGPQDRLRALVVIPIIFGILFA----
                                                                                                                                                                                                                                                                                         CESCVLHRSCSPGFGVKQIATGVSDTICEPCPVGFFSNVSSAFEKCHPWTSCETKDLVVQ 175
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                                                                                                                                                                                                                                                                                                                                                                           CLPCGESEFLDTWNRETHCHQHKYCDPNLGLRVQQKGTSETDTICTCEEGWHC---TSEA 115
                 rabbit fibroma virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17.0%; Score 267.5; DB 2; 26.1%; Pred. No. 1.2e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50;
                                                                                                                                                               -TTVAVEETI 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches 116;
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A; Dualus, Frontain
A; Molecule type: mRNA; protein
A; Residues: 23-461 <DEM>
A; Cross-references: GB:S63368; NID:g235648; PIDN:AAB19824.1; PID:g235649
A; Cross-references: GB:S63368; NID:g235648; PIDN:AAB19824.1; PID:g235649
A; Cross-references: GB:S63368; NID:g235648; PIDN:AAB19824.1; PID:g235649
                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-195, 'R', '197-461 <KOH>
A; Cross-references: GB: M55994; GB: M38549; NID: g339757; PIDN: AAA36755.1; PID: g339758
A; Cpembic, Z.; Loetscher, H.; Gubler, U.; Pan, Y.C.; Lahm, H.W.; Gentz, R.; Brockhaus
Cytokine 2, 231-237, 1990
                                                                                                                                                                                                          A; Title: Two human TNF receptors have similar extracellular, A; Reference number: A48416; MUID:91370690
                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:M32315; NID:g189185; PIDN:AAA59929.1; PID:g189186 R;Kohno, T.; Brewer, M.T.; Baker, S.L.; Schwartz, P.E.; King, M.W.; Hale, Proc. Natl. Acad. Sci. U.S.A. 87, 8331-8335, 1990 A;Tille: A second tumor necrosis factor receptor gene product can shed a A;Reference number: A36475; MUID:91045991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Reference number: A35356; MUID:90260639
A;Accession: A35356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 08-Dec-2000
C;Accession: A35356; A36475; A48416; A36007; A23666; B35010; I38094
R;Smith, C.A.; Davis, T.; Anderson, D.; Solam, L.; Beckmann, M.P.; Jerzy, R
Science 248, 1019-1023, 1990
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C;Superfamily: myxoma virus T2 protein; NGF receptor repeat homology
F;64-105/Domain: NGF receptor repeat homology <NG2>
F;106-147/Domain: NGF receptor repeat homology <NG3>
                                                                                                                                               A; Status: preliminary
                                                                                                                                                                         A; Accession: A48416
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A; Residues: 1-461 <SMI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tumor necrosis factor receptor 2 precursor [validated] - human N; Alternate names: 75K tumor necrosis factor receptor; TNF receptor type
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A;Molecule type: DNA
A;Residues: 1-325 <UPT>
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C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
                                                                                                                                                                                                    A; Reference number: A48416;
                                                                                                                                                                                                                                                                                                                                                                                                     A; Status: preliminary
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A; Accession: B43692
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Best Local Similarity
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31.5%;
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Pred. No. 4.8e-12;
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A;Title: Cloning, sequencing and partial functional characterization A;Title: Cloning, sequencing and partial functional characterization
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A; Nolecule type: protein
A; Residues: 23-40;65-69;136-141;300-306 <LOE>
A; Residues: ". Novick. D.; Wallach, D.
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A;Title: Complementary DNA cloning of a receptor for tumor necrosis factor and A;Reference number: A36007; MUID:90349572
A;Accession: A36007
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J. Biol. Chem. 265, 1531-1536, 1990
A;Title: Two tumor necrosis factor-binding proteins
A;Reference number: A35010; MUID:90110215
hypothetical
                            T28623
                                                 RESULT
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A; Residues: 1-37 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: protein A; Residues: 27-31 <ENG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: GDB:TNFR2
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Best Local Similarity
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164-201/Domain: NGF receptor repeat homology <NG4>
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                                                 u
                                                                                                                                                                           PGQRVQKGGTESQDTLCQNCPPGTFS-PNGTLEECQHQTKCSWLVTKAGAG-----TSSS 199
                                                                                                                                                                                                                            ECLSC-----GSRCSSDQVETQACTREQNRICTCRPGWYCALSKQEGCRLCAPLRKCR 144
                                                                                                                                                                                                                                                                           KCLQCQMCDPAMGLRASRN-----CSRTENAVCGCSPGHFCIVQDGDHCAACRAYATSS 145
                                                                                                                                                                                                                                                                                                                            YAPEPGSTCRLREYYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDSCEDSTYTQLWNWVP 91
                                                                                                                                                                                                                                                                                                                                                         YAPALPS-CKEDEY--PVGSECCPKCSPGYRVKEACGELTGTVCEPCPPGTYIAHLNGLS 91
                                                                                                                            PGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICRPHQICNVVAIPGNASMDAVCTSTS
protein
                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      site: carbohydrate (Asn) (covalent) #status
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  G2R -
                                                                                                                                                                                                                                                                                                                                                                                                                                                      16.4%;
variola major virus
                                                                                                                                                                                                                                                                                                                                                                                                                               23;
                                                                                                                                                                                                                                                                                                                                                                                                                            Score 259; DB 1;
Pred. No. 7.7e-12;
3; Mismatches 76
                                                                                                                                                                                                                                                                                                                                                                                                                               76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       purified from human urine. Evidence
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C;Species: variola major virus
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 21-Jul-2000
C;Accession: T28623
R;Massung, R.F.; Esposito, J.J.; Liu, L.I.; Qi, J.; Utterback, T.R.; Knight
Nature 366, 748-751, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            submitted to GenBank, March 199
A;Description: Analysis of the
A;Reference number: A72150
A;Accession: D72175
                                                                                                                                                                                                                                                                                                                                         A;Gene: G2R
C;Superfamily: myxoma virus T2 protein; NGF receptor repeat homology
                                                                                                                                                                                                                                                                                                                                                                              C; Genetics:
A; Gene: G2R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        G2R protein - variola minor virus (strain Garcia-1966)
C;Species: variola minor virus
C;Date: 24-Nov-1999 #sequence_revision 24-Nov-1999 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:L22579; NID:g623595; PIDN:AAA60933.1; PID:g439102
A;Experimental source: strain Bangladesh 1975
C;Superfamily: myxoma virus T2 protein; NGF receptor repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: Potential virulence determinants in terminal regions of variola smallpox vir A;Reference number: 220488; MUID:94088747 A;Accession: T28623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Shchelkunov,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
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130
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                                                                                                                                                                                        21 LRLVLYLTFLGAPC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 NTQCTPCGSGTFTSRNNHLPACLSCNGRCN--SNQVETRSCNTTHNRICECSPGYYCLLK 118
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                                                                                                                                                                                                                                                             Local
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QDGDHCAACRAYATSSPGQRVQKGGTESQDTLCQNCPPGTFS-----PNGTLE 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IDVEITLYPVNDTSCTRTTT---TGLSES----ILTSELTITM 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GSSGCKACVSQTKCGIGYGV-SGHTSVGDVICSPCGFGTYSHTVSSADKCEPVPNNTFNY 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTVCEPCPPGTYIAHLNGLSKCLQCQ-MCDPAMGLRASRNCSRTENAVCGCSPGHFCIVQ 130
                                                                                                                                            MKSVLYLYILFLSCIIINGRDAAPYTPPNGKCKDTEYKRHNLCCLSCPPGTYASRLCDSK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MKSVLYLYILFLSCIINGRDAAPYTPPNGKCKDTEYKRHNLCCLSCPPGTYASRLCDSKT
                                              TNTQCTPCGSGTFTSRNNHLPACLSCNGRCN--SNQVETRSCNTTHNRICECSPGYYCLL 118
                                                                                             TGTVCEPCPPGTYIAHLNGLSKCLQCQ-MCDPAMGLRASRNCSRTENAVCGCSPGHFCIV 129
                                                                                                                                                                                                                                       66; Conser
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                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                             16.3%;
29.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complete coding sequence of DNA of alastrim variola
                                                                                                                                                                       ---YAPALPSCKEDEYPVGSECCPKCSPGYRVKEACGEL 70
                                                                                                                                                                                                                                       23;
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                                                                                                                                                                                                                                    Score 257; DB 2;
Pred. No. 8.5e-12;
3; Mismatches 94
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}; Mismatches
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Pred. No. 7.
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nes 94;
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A;Experimental source: strain India-1967, ssp. major, isolate Ind3
A;Experimental source: strain India-1967, ssp. major, isolate Ind3
R;Kolykhalov, A.A.; Blinov, V.M.; Gytorov, V.V.; Pozdnyakov, S.G.; Chizhikov, V.E.; submitted to the EMBL Data Library, April 1992
A;Description: Nucleotide sequence analysis of the region of Variola virus XhoI F O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N;Alternate names: B28R protein (COP)
C;Speciles: variola virus
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 23-Mar-2001
C;Accession: D36858; S46888; S32385; S35987
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C; Genetics:
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A; Residues: 31-168 <SHC>
A; Cross-references: EMBL: X69198
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A; Accession: S32385
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A; Molecule type: DNA
A; Residues: 1-349 <KOL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEBS Lett. 319, 80-83, 1993
A;Title: Genes of variola and vaccinia viruses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R; Shchelkunov, S.N.; Blinov, V.M.; Sandakhchiev,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:X67117; NID:g516428; PIDN:CAA47540.1; A;Experimental source: strain India-1967, isolate Ind3
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A; Status: preliminary
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Best Local
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                  necrosis
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                                                                                                                                       178 YIDVEITLYPVNDTSCTRTTT-
                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 LRLVLYLTFLGAPC-----YAPALPSCKEDEYPVGSECCPKCSPGYRVKEACGEL 70
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                                                                                                                                                                                                                            KGSSGCKACVSQTKCGIGYGV-SGHTSVGDVICSPCGFGTYSHTVSSADKCEPVPNNTFN
                                                                                                                                                                                                                                                                                                                 THTQCTPCGSGTFTSRNNHLPACLSCNGRCN--SNQVETRSCHTTHNRICECSPGYYCLL 118
                                                                                                                                                                                                                                                                                                                                                                                                         MKSVLYLYILFLSCIIINGRDAAPYTPPNGKCKDTEYKRHNLCCLSCPPGTYASRLCDSK 60
                                                                                                                                                                                                                                                                    QDGDHCAACRAYATSSPGQRVQKGGTESQDTLCQNCPPGTFS------PNGTLE 177
                                                                                                                                                                                                                                                                                                                                                              TGTVCEPCPPGTYIAHLNGLSKCLQCQ-MCDPAMGLRASRNCSRTENAVCGCSPGHFCIV 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                               -----HQTKCSWLVTKAGAGTSSSHWVWWFLSGSLVIVI 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        source: strain India-1967, ssp. major
                     tactor
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                  receptor
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                  2-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23;
                                                                                                                                    ---TGLSES----ILTSELTITM 214
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No. 8.
                  protein
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}.5e-12;
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A:Cross-references: EMBL:X17037; NID:g57830; PIDN:CAA34897 C;Superfamily: CD27 antigen; NGF receptor repeat homology C;Keywords: growth factor receptor; transmembrane protein F;1-19/Domain: signal sequence #status predicted <SIG>F;20-271/Product: OX40 antigen #status predicted <MAT>F;211-235/Domain: transmembrane #status predicted <TMM>
                                                                                                                                                                                                                                                   N;Alternate names: nerve growth factor receptor homolog C;Species: Rattus norvegicus (Norway rat) C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text C;Accession: S12783; S08036 R;Mallett, S.; Fossum, S.; Barclay, A.N. EMBO J. 9, 1063-1068, 1990
                                                                                                                                                                                   A; Title: Characterization of the MRC OX40 A; Reference number: S12783; MUID:90214614 A; Accession: S12783
                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-271 <MAL>
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A;Map position: 12p13.3-12p13.1
C;Superfamily: tumor necrosis factor receptor type 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genomics 16, 214-218, 1993

A; Title: Construction and evaluation of a hncDNA library of human 12p transcribed seq A; Reference number: I54182; MUID:93252381

A; Accession: I54182
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C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 17-Mar-2000
C;Accession: I54182
R;Baens, M.; Chaffanet, M.; Cassiman, J.J.; Van den Berghe, H.; Marynen, P.
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A;Cross-references:
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-435 < RE
                                                                                                                                                                                                                                                                                                                                                                                       OX40 antigen precursor - rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: preliminary; translated from GB/EMBL/DDBJ
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --PDVTTVAVEETIPSFTGRSP 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VIVCSTVGLII------CVKRRKPRGDVVKVIVSVQRKRQEAEGEATVIEALQAP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PPGTF----SPNGTLEECQHQTKC-SWLVTKAGAGTSSSHWVWW-------FLSGSLVI 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ECCPKCSPGYRVKEACGELTGTVCEPCPPGTYIAHLNGLSKCLQCQMCDPAMGLRASRNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PG-DWGPPPWRSTPRTDVLRLVLYLTFL-----GAPCYAPALPSCK--EDEY--PVGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KAGHFQNTSSPSA---RCQPHTRCENQGLVEAAPGTAQSDTTCKNPLEPLPPEMSGTMLM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86;
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2rences: GB:L04270; NID:g339761; PIDN:AAA36757.1;
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26.7%;
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Pred. No. 2e-11;
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                                                                                                                   PID:957831
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Query Match

Similarity

15.2%;

Conservative

16;

Mismatches

54;

Indels

25;

Gaps

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Pred. No. Score

1.1e-10;

240.5;

ĎВ 2;

Length 271;

Matches Best Local

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RESULT 10
GQVZML
T2 protein -
                                                         C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 11-Jan-2000
C;Accession: 148700; 14834; S34377
R;Calderhead, D.M.; Buhlmann, J.E.; van den Eertwegh, A.J.; Claassen, E.; Nd. Immunol. 151, 5261-5271, 1993
A;Title: Cloning of mouse 0x40: a T cell activation marker that may mediate A;Reference number: 148700; MUID:94044750
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                                                                                                                                                                                                                                                                                           gene ox40 protein - mouse N;Alternate names: OX40 antigen
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F;64-105/Domain: NGF receptor repeat homology <NG2>
F;106-147/Domain: NGF receptor repeat homology <NG3>
F;66,181,205,238/Binding site: carbohydrate (Asn) (co
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A; Residues: 1-326 < UPT>
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C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 18-Jun-1999
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                          A; Accession: I48700
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 VLRLVLYLTFL-----GAPCYAPALPSCKEDEYPVGSECCPKCSPGYRVKEACGELTGT 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DRYQNTTKMCTLNIEIRCVE----GDAVRTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---LVIVIVCSTVGLIICVKRRKPRGDVVKVI 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DHCAACRAYATSSPGQRVQKGGTESQDTLCQNCPPGTFSPN-GTLEECQ------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VCEPCPPGTYIAHLNGLSKCLQCQ-MCDPAMGLRASRNCSRTENAVCGCSPGHFCIVQDG 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MFRLTLLLAYVACVYGGGAP-YGADRGKCRGNDYEKDGLCCTSCPPGSYASRLCGPGSDT 59
translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----HQTKCSWLVTKAGA------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EGCRIC-APKTKCPAGYGVSGHTRTGDVLCTKCPRYTYSDAVSSTETCTSSFNYISVEFN 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VCSPCKNETFTASTNHAPACVSCRGRC--TGHLSESQSCDKTRDRVCDCSAGNYCLLKGQ 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PAMGLRASRNCSRTENAVCGCSPGHFCIVQDGDHCAACRAYATSSPGQRVQKGGTESQDT 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SCKEDEYPVGSECCPKCSPGYRVKEACGELTGTVCEPCPPGTYIAHLNGLSKCLQCQMCD 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -CVPCPPGHESP-GSNQACKPWINCI 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LCONCPPGTFSPNGTLEECQHQTKCS 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HRSGSELKQNCTPTEDTVCQCRPG-TQPRQDSSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCVKDTYPSGHKCCRECQPGHGMVSRCDHTRDTVCHPCEPGFYNEAVN-YDTCKQCTQCN 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     l Similarity
73; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A40566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       myxoma virus (strain Lausanne)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J.L.; Schreiber, M.; Mcfadden,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -TTAGPNEVVKTSEFSVTLNHTDCDPVFHTEYYGTSGSEGAGGFFTGM 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15.1%;
                                                                                                                                                           J.E.; van den Eertwegh, A.J.; Claassen, E.; Noelle,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 238.5; Pred. No. 1.8e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein with homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Asn) (covalent) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .8e-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -GTSSSHWVWWFLSGS 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6
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                                                                                              T-B
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                                                                                              cell int
                                                                                                                                                              R.J.;
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                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                    A; Reference number: S54816
A; Accession: S54816
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A; Residues: 1-474 <GOO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Residues: 1-14, 'G', 16-272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
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Best Local
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A; Nedecule type: DNA
A; Residues: 1-22 <KIS>
A; Residues: 1-22 <KIS>
A; Residues: 1-22 <KIS>
A; Cross-references: EMBL: X87128; NID: g809043; PIDN: CAA60618.1; PID: g809044
A; Cross-references: EMBL: X87128; NID: g809043; PIDN: CAA60618.1; PID: g809044
C; Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology
C; Keywords: cytokine receptor; transmembrane protein
F; 1-22/Domain: signal sequence #status predicted <SIG>
F; 1-22/Domain: tumor necrosis factor receptor type 2 #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Goodwin, R.G.; Anderson, D.; Jerzy, R.; Mol. Cell. Biol. 11, 3020-3026, 1991 A;Title: Molecular cloning and expression A;Reference number: A40254; MUID:91246168 A;Accession: A40254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-474 < LEW>
A; Cross-references: GB: M60469; NID: g199827; PIDN: AAA39752.1; PID: g199828
A; Cross-references: GB: M60469; NID: g199827; Davis, T.; Brannan, C.I.; Cope
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R; Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991.
A;Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis facto A; Reference number: A38634; MUID:91187885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999
C;Accession: B38634; A40254; S54816
                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:M60469; NID:g199827; PIDN:AAA39752.1; PID:g199828 R;K1ssonerghis, M.; Fellowes, R.; Feldmann, M.; Chernajovsky, Y. submitted to the EMBL Data Library, May 1995 A;Description: Characterization of the promoter region of the murine p75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tumor necrosis factor receptor type 2 precursor -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:X85214; NID:g732818; PIDN:CAA59476.1;
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A; Residues: 1-272 <RES>
79-120/Domain: NGF receptor repeat homology <NG2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    161 LCQNCPPGTFSPNGTLEECQHQTKCS 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85 HRSGSELKQNCTPTQDTVCRCRPG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41 SCKEDEYPVGSECCPKCSPGYRVKEACGELTGTVCEPCPPGTYIAHLNGLSKCLQCQMCD 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -CVPCPPGHFSP-GNNQACKPWTNCT 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86/1; 122/1; 144/2; 210/1;
D27 antigen; NGF receptor re
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Pred. No. 7.5e-09;
7; Mismatches 58
                                                                                                                                                                                                                                                                                                                                                                                                                                    promoter region of the murine p75-TNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of the type 1 and type 2
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homology <NG4>

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A;Title: A variant mRNA species encoding a tr
A;Reference number: JC2395; MUID:94128114
A;Accession: JC2395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999
C;Accession: 148854
R;Fowell, E.E.; Wicker, L.S.; Peterson, L.B.; Todd, J.A.
Mamm. Genome 5, 726-727, 1994
A;Title: Allelic variation of the type 2 tumor necrosis factor receptor gend A;Reference number: 148854; MUID:95178848
A;Accession: 148854
                                                                                                                   C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change
C;Accession: JC3395; PC2246
R;Kimura, K.; Wakatsuki, T.; Yamamoto, M.
Biochem. Biophys. Res. Commun. 198, 666-674, 1994
                                                                                                                                                                                                                                                                                                                                                                                                          В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:X76401; NID:g433830; PIDN:CAA53981.1; PID:g433831 C;Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat F;151-188/Domain: NGF receptor repeat homology <NGF>
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A;Cross-references: DDBJ:D26112; NID:g468486; PIDN:BAA05108.1;
                       A; Residues: 1-324 <KIM>
                                       A; Molecule type: mRNA
                                                                                                                                                                                                                      Fas antigen precursor - rat
                                                                                                                                                                                                                                               JC2395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SILAIPGNASTDA 200
                                                                                                                                                                                                                                                                                                                              SDTTSSTDVCRPHRICSILAIPGNASTDA 185
                                                                                                                                                                                                                                                                                                                                                                S-PNGTLEECQHQTKCSWLVTKAGAGTSS
                                                                                                                                                                                                                                                                                                                                                                                                          TKQQNRVCACEAGRYCALKTHSGSCRQCMRLSKCGPGFGVASSRAPNGNVLCKACAPGTF 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SRTENAVCGCSPGHFCIVQ-DGDHCAACRAYATSSPGQRVQKGGTESQDTLCQNCPPGTF 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCAKCPPGQYVKHFCNKTSDTVCADCEASMYTQVWNQFRTCLSCSSSC--STDQVETRAC 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SWLVTKAGAGTSS 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IVQ-DGDHCAACRAYATSSPGQRVQKGGTESQDTLCQNCPPGTFS-PNGTLEECQHQTKC 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VFELQLWATGHTVPAQVVLTPYKPEPGYECQISQEYYDRKAQMCCAKCPPGQYVKHFCNK 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VLRLVLYLTFLGAPCYAPALPSCKEDEY -- PVGSE------CCPKCSPGYRVKEACGE
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Pred. No. 1.
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  PID:d1005650; PID:g468487
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J. Biol. Chem. 267, 10709-10715, 1992
A;Title: Purification and molecular cloning of A;Reference number: A38142; MUID:92268122
A;Accession: A38142
A;Status: preliminary; not compared with concel A;Molecule type: nucleic acid A;Molecule type: nucleic acid A;Molecule type: SW6.4 Cells
A;Note: sequence extracted from NCBI backbone A;Note: in NCBI backbone the source is designated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Introns: 62/1
C; Superfamily: N
C; Keywords: trar
                                                                                                                                                                                                                                                                                                                                                                           R;Krammer, P.H.
submitted to the EMBL Data Library, February 1992
A:Reference number: S24543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A:Experimental source: thymus
A;Accession: PC2246
A;Molecule type: mRNA
A;Residues: 1-62,'RFT' <KI2>
A;Cross-references: DDBJ:D26113;
                                                                                                                                                                                                                   A;Cross-references: EMBL:X63717; NID:g28741; PID:g28742 R;Oehm, A.; Behrmann, I.; Falk, W.; Pawlita, M.; Maier, J. Biol. Chem. 267, 10709-10715, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cell 66, 233-243, 1991
A;Title: The polypeptide encoded by the cDNA for human cell surface antigen Fas can
A;Reference number: A40036; MUID:91309137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Homo sapiens (man)
C;Date: 17-Jan-1992 #sequence_revision 17-Jan-1992 #text_change 21-Jul-2000
C;Accession: A40036; 524543; A38142
R;Itoh, N,; Yonehara, S.; Ishii, A.; Yonehara, M.; Mizushima, S.I.; Sameshi
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C; Genetics:
                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-335 < KRA>
                                                                                                                                                                                                                                                                                                                                                                    A; Reference number: A; Accession: S24543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-335 < ITO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCSEGLYQVGPFCCQPCQPGERKVKDCTTSGGAPTCHPCTEGEEYTDRKHYSDKCRRCAF 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SCKEDEYPVGSECCPKCSPGYRVKEACGELTGT-VCEPCPPG-TYIAHLNGLSKCLQCQM 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NTKCKK--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58;
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  extracted from NCBI backbone (NCBIP:103810) backbone the source is designated as mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                         conceptual translation
                                                                                                                                                                                                  of the APO-1 cell surface antigen,
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                                                                                                                                                                                                                                               C.; Li-Weber, M.;
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C;Genetics:
A;Gene: GDB:APT1
A;Cross-references: GDB:132671; OMIM:134637
A;Map position: 10q24.1-10q24.1
C;Superfamily: NGF receptor repeat homology
C;Keywords: apoptosis; surface antigen; transmembrane protein F;1-16/Domain: signal sequence #status predicted <SIG>F;85-18/Domain: NGF receptor repeat homology <NG4>F;85-18/Domain: signal sequence #status predicted <TMM>
Search completed: January 24, 2002, 16:22:25 Job time: 75 sec
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                                                                                                    139 VCEHCDPCTKCEHGIIKECTLTSNTKC----KEEGSRSNLGW---
                                                                                                                                                                                                                                        161 LCQNCPPGTFSPNGTLEEC--QHQTKCSWLVTKAGAGTSSSHWVWWFLSGSLVIVIVCST 218
                                                                                                                                                                                                                                                                                      109 EGHGLEVEINCTRTQNTKCRCKPNFFC-----138
                                                                                                                                                                                                                                                                                                                               101 PAMGLRASRNCSRTENAVCGCSPGHFCIVQDGDHCAACRAYATSSPGQRVQKGGTESQDT 160
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    January 24, 2002, 16:22:05; Search time 9.87 Seconds (without alignments) 1051.281 Million cell updates/sec
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CD40_BOVIN
VT2_SFVKA
               TNR1_PIG
TNR1_BOVIN
CD27_MOUSE
TNR1_MOUSE
41BB_HUMAN
CD30_HUMAN
TNR1_HUMAN
                                                                                                                                      FASA_HUMAN
FASA_MOUSE
NGFR_RAT
FASA_BOVIN
NGFR_CHICK
OX40_HUMAN
TNR1_RAT
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OX40_RAT
VT2_MYXVL
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TNR2_MOUSE
FASA_RAT
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CD40_MOUSE
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41BB_MOUSE
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Compugen Ltd.
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9 rattus norv
8 h wsl-1 pro
5 homo sapien
6 mus musculu
4 rattus norv
7 bos taurus
9 gallus gall
9 homo sapien
4 rattus norv
8 homo sapien
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3 shope fibro
3 homo sapien
5 variola vir
1 homo sapien
4 mus musculu
5 rattus norv
s sus scrofa
bos taurus
bos taurus
mus musculu
mus musculu
mus musculu
momo sapien
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mus musculu
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133.5 8.8 5376 1 ZAN MOUSE 139.5 8.8 5376 1 ZAN MOUSE 133.5 8.5 4393 1 PGBM_HUMAN 130.5 8.3 1786 1 LMB1_MOUSE 127.5 8.1 3707 1 PGBM_MOUSE 126 8.0 1557 1 LML1_CAEEL 126 8.0 1557 1 LML2_CAEEL 126 8.0 1798 1 LMB2_HUMAN 125 7.9 722 1 DLL1_MOUSE 122 7.7 714 1 DLL1_RAT 122 7.7 1964 1 LMA2_MOUSE 121.5 7.7 1964 1 LMA2_MOUSE 121.5 7.7 1964 1 LMC4_MOUSE 121.5 7.7 1964 1 LMC4_MOUSE 121.7 7.5 1 COMP_RAT	9.1 1786 1 LMB1_HUMAN 8.8 5376 1 ZAN_MOUSE 8.5 4393 1 PGBM_HUMAN 8.3 1786 1 LMB1_MOUSE 8.1 3707 1 PGBM_MOUSE 8.1 3707 1 PGBM_MOUSE 8.0 1557 1 LML1_CAEEL 8.0 1798 1 LMB2_HUMAN 7.9 722 1 DLL1_MOUSE 7.7 714 1 DLL1_RAT 7.7 3106 1 LMA2_MOUSE 7.7 1964 1 NTC4_MOUSE 7.7 755 1 COMP_RAT	45	44	43	42	41	40	39	38	37	36	3 5	34
1786 14393 14393 1786 1786 1557 1798 1798 1724 1724 13106 11964 1755	1786 1 LMBI_HUMAN P07942 5376 1 ZAN_MOUSE 088799 4393 1 PGBM_HUMAN P02469 1786 1 LMBI_MOUSE P98160 3707 1 PGBM_MOUSE Q05793 1557 1 LMLI_CAEEL Q1892 1758 1 LMBZ_HUMAN P55268 722 1 DLLI_MOUSE Q61483 714 1 DLLI_MOUSE P7577 3106 1 LMAZ_MOUSE P97677 3106 1 LMAZ_MOUSE P31695 755 1 CONP_RAT P35444	121	121.5	122	122	125	126	126	127.5	130.5	133.5	139.5	143.5
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1 LMS1_HUMAN 1 ZAN_MOUSE 1 ZAN_MOUSE 1 PGBM_HUMAN 1 LMB1_MOUSE 1 PGBM_MOUSE 1 LML1_CAEEL 1 LMB2_HUMAN 1 DLL1_MOUSE 1 DLL1_RAT 1 LLA2_MOUSE 1 LMA2_MOUSE 1 NTC4_MOUSE 1 NTC4_MOUSE	P0/942 ORB/99 P98160 P02469 Q05793 Q18023 P55268 Q61483 P97677 Q60675 P31695	755	1964	3106	714	722	1798	1557	3707	1786	4393	5376	1786
LMB1_HUMAN ZAN_MOUSE PGBM_HUMAN LMB1_MOUSE LMB1_CAEEL LMB2_HUMAN DLL1_ROUSE DLL1_ROT LMB2_MOUSE DLL1_RAT LMA2_MOUSE COMP_RAT COMP_RAT	P0/942 ORB/99 P98160 P02469 Q05793 Q18023 P55268 Q61483 P97677 Q60675 P31695	_	_	_	_		_	ш	سو	<u>, , , , , , , , , , , , , , , , , , , </u>	Н	μ.	
		COMP_RAT	NTC4_MOUSE	LMA2_MOUSE	DLL1_RAT	DLL1_MOUSE	LMB2_HUMAN	LML1_CAEEL	PGBM_MOUSE	LMB1_MOUSE	PGBM_HUMAN	ZAN_MOUSE	LMB1_HUMAN

ALIGNMENTS

RESULT 1

TR14_HUMAN STANDARD; PRT;

AC Q92956; Q9UM65;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last superpantly MEMBER 14 PRECURSOR
DT TUMOR NECROSIS FACTOR RECEPTOR SUPERPANTLY MEMBER 14 PRECURSOR
DE TUMOR NECROSIS ENTRY MEDIATOR) (TUMOR NECROSIS FACTOR RECEPTOR-LIKE:

2)

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CD27_HUMAN

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RESULT
CD40_MC
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Best Local Similarity
       Mus musculus (Mouse).
Eukaryota; Metazoa; C
Mammalia; Eutheria; R
NCBI_TaxID=10090;
                                                              CD40_MOUSE
P27512;
01-AUG-1992
01-OCT-1996
15-JUL-1999
                                                                                                                _MOUSE
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DISULFID
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                                             TNFRSF5 OR CD40
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SMART; SM00208; TNFR; 3.
PROSITE; PS006655
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REPEAT
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MIM; (
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                                                                                                                                                    CSPGHFCIVQDGDHCAACRAYATSSPGQRVQKGGTESQDTLCQNCPPGTFSPNGTLEECQ
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                                                                                                                                                                                                                                                                                                                     MEPPGDWGPPPWRSTPRTDVLRLVLYLTFLGAPCYAPALPSCKEDEYPVGSECCPKCSPG
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                                                                                                                                                                                                     HQTKCSWLVTKAGAGTSSSHWVWWFLSGSLVIVIVCSTVGLIICVKRRKPRGDVVKVIVS
                                                                                                                                                                                                                                CSPGHFCIVQDGDHCAACRAYATSSPGQRVQKGGTESQDTLCQNCPPGTFSPNGTLEECQ
                                                                                                                                                                                                                                                                      YRVKEACGELTGTVCEPCPPGTYIAHLNGLSKCLQCQMCDPAMGLRASRNCSRTENAVCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transmembrane;
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                                                               (Rel. 23, Created)
(Rel. 34, Last sequence update)
(Rel. 38, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                   Conservative
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203
224
42
42
78
121
121
138
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173
                                   (Mouse)
                                                    el. 38, Last annotation update)
PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (BP50) (CDW40)
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                                                                                                       STANDARD;
                 Chordata;
Rodentia;
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99.6%;
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DOT
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Pred. No. 5e-120;
1; Mismatches
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3 X TNFR-CYS.
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                Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                       PRT;
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                                                                                                                                                                                                                                                                                                                                                                    DB 1;
                                                                                                                                                                                                                                                                                                                                                 0,
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DOMAIN
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pfam; PF00020; TNER_C6; 4.
proDom; PD000771; TNER_C6; 1.
smart; SM00208; TNER; 4.
prOSITE; PS00652; TNER_NGER_1; 1.
prOSITE; PS50050; TNER_NGER_2; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=93094586; PubMed=1281194; Grimaldi J.C., Torres R., Kozak C.A., Howard M., Cockayne D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-92105763; PubMed-1370315;
Torres R.M., Clark E.A.;
"Differential increase of an alternatively polyadenylated mRNA species of murine CD40 upon B lymphocyte activation.";
"Immunol. 148:620-626(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Receptor;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (S or send an email to license@isb-sib.ch).
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MGD; MGI:88336; Tnfrsf5
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-!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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161
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                                        85
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LCQNCPPGTFSPNGTL-EECQHQTKCS----WLVTKAGAGTSSSHWVWWFLSGSLVIVIV
                                      PNQGLRVKKEGTAESDTVCTCKEGQHCTSKD---CEACAQHTPCIPGFGVMEMATETTDT
                                                                            PAMGLRASRNCSRTENAVCGCSPGHFCIVQDGDHCAACRAYATSSPGQRVQKGGTESQDT 160
                                                                                                                       TCSDKQYLHDGQCCDLCQPGSRLTSHCTALEKTQCHPCDSGEFSAQWNREIRCHQHRHCE
                                                                                                                                                             SCKEDEYPVGSECCPKCSPGYRVKEACGELTGTVCEPCPPGTYIAHLNGLSKCLQCQMCD 100
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194
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104
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27.9%;
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                                                                                                                                                                                                                                                                                                            WW.
                                                                                                                                                                                                      43;
                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
CYTOPLASMIC (POTENTIAL).
4 X THER-CYS.
THER-CYS 1.
THER-CYS 3.
THER-CYS 3.
THER-CYS 4.
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Pred.
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; C791CB6D2FEA574E CRC64
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EXTRACELLULAR (POTENTIAL).
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                                                                                                                                                                                                        Mismatches
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No. 1.9
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MBL outstation -
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CD40_HUMAN
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P25942;
01-MAY-1992
                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                               ProDom; PD000771; TNFR_c6; 1. SMART; SM00208; TNFR; 4.
                                                               InterPro; IPR001368; TNFR_c6
Pfam; PF00020; TNFR_c6; 4.
                                                                                                                                                                             or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                        Zheng Z., Naismith J.H., Thomas D.;
"The role of polar interactions in the molecular recognition of CD40L with its receptor CD40.";
Protein Sci. 7:1124-1135(1998).
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Singh J., Garber E., van Vlijmen H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "A B-lymphocyte activation molecule relat
factor receptor and induced by cytokines
EMBO J. 8:1403-1410(1989).
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01-MAY-1992 (Rel.
30-MAY-2000 (Rel.
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                                                                                               мім; 109535;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=97189482;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Construction and analysis of a detailed three-dimensional model the ligand binding domain of the human B cell receptor CD40."; proteins 27:59-70(1997).
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                                                                                                                                                                                                                                                                                                      SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION DATABASE: NAME-PROW; NOTE-CD guide CD40 entry; WWW-"http://www.ncbi.nlm.nlh.gov/prow/cd/cd40.htm".
                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
TISSUE SPECIFICITY: B-CELLS AND IN PRIMARY CARCINOMAS
                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L
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                                                                                                                                 S04460;
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                                                                                                               1CDF; 01-APR-97
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S04460; S04460.
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TNFR_NGFR_1;
TNFR_NGFR_2;
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PubMed=9037712;
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Last annotation update)
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CD40_BOVIN
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Best Local
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Q28203;
Q1-NOV-1997 (Rel. 3
01-NOV-1997 (Rel. 3
15-JUL-1999 (Rel. 3
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                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute. Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
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REPEAT
                   homologue:
cattle.";
                          Hirano A., Brown W.C., Estes D.M.; "Cloning, expression and biological function of the bovine homologue: role in B-lymphocyte growth and differentiation
                                                                                                                                    CD40L RECEPTOR PRECURSOR TNFRSF5 OR CD40.
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Immunology 90:294-300(1997)
-i- FUNCTION: RECEPTOR FOR A
                                                        MEDLINE=97281252;
                                                                  SEQUENCE FROM
                                                                                   NCBI_TaxID=9913;
                                                                                                                           Bos taurus (Bovine).
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                                                                                                                                                                                                                                             226
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                                                                 N.A.
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26.1%;
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Last annotation update)
SOR (B-CELL SURFACE ANTI
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A CYTOKINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 267.5; I
Pred. No. 9.6e<sup>o</sup>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
BC8776EC2C4A5680 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TNFR-CYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TNFR-CYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 X TNFR-CYS.
TNFR-CYS 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
CD40L RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EXTRACELLULAR
                                                                                                                                                                                              PRT;
                                                                                                                                                                                              269
                                                                                                                                                                                                                                             255
 LIGAND KNOWN
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                                                                                                                                             ANTIGEN
                                                                                                                                                                                              A
                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                           116;
                                                                                                                                                                                                                                                                                  - ILLVLVFIKKVAKKPTNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Repeat; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CRC64;
                                                                                                                                             CD40) (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
 AS CD40L
                                                                                                                 Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             277;
                                                                                                         Bovoidea
                                                                                                                                                                                                                                                                                                                                                                                                                                          35;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                     251
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VT2_SFVA

ID VT2_S

AC P2594

DT 01-MA

DT 01-MA

DT 15-JU

DE TUMOR

GN T2.

OS Shope

OC Lepor

OX NCBI.

RN (EU.
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Best Local Similarity
                                                                                                                                                                                                                                                                                       VT2_SFVKA
P25943;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
NON_TER
SEQUENCE
SEQUENCE FROM N.A.
MEDLINE-87321103; PubMed=2820128
                                                                     Leporipoxvirus.
NCBI_TaxID=10272;
                                                                                                                    Viruses; dsDNA viruses,
                                                                                                                                            Shope fibroma virus
                                                                                                                                                                                           TUMOR NECROSIS
                                                                                                                                                                                                               01-MAY-1992 (Rel. 22,
01-MAY-1992 (Rel. 22,
15-JUL-1999 (Rel. 38,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Receptor; SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bloinformatic lines as long as its concent use by non-profit institutions as long as its concent usage by and for commercial modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPRO01368; TNFR_c6. pfam; PF00020; TNFR_c6; 4. ProDom; PD000771; TNFR; 6; 1. SMART; SM00208; TNFR; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U57745; AAC48710.1; -. HSSP; P25942; ICDF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSMEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00652; TNFR_NGFR_1; 1. PROSITE; PS50050; TNFR_NGFR_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REPEAT
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SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VLRLVLYLTELG---APCYAPALPSCKEDEYPVGSECCPKCSPGYRVKEACGELTGTVCE 76
                                                                                                                                                                                                                                                                                                                                                                                                                                   GTNKTDVVCGFQSRMRTLVVIPVTMGVLFAVLL-----VSACIRNITKKRQ 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTSSSHWVWWFLSGSLVIVIVCSTVGLIICVKRRKPRGDVVKVIVSVQRKRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SCTPHSLCLPGFGVKQIATGLLDTVCEPCPLGFFSNVSSAFEKCHRWTSCERKGLVEQHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACRAYATSSPGQRVQKGGTESQDTLCQNCPPGTFS-PNGTLEECQHQTKCSWL-VTKAGA 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SCGKGEFLSTWNREKYCHEHRYCNPNLGLRIQSEGTLNTDTICVCVEGQHC---TSHTCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PCPPGTYIAHLNGLSKCLQCQMCDPAMGLRASRNCSRTENAVCGCSPGHFCIVQDGDHCA 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MVRLPLQCLFWGFFLTAVHSEPATACGEKQYPVNSLCCDLCPPGQKLVNDCTEVSKTECQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B-cell; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                              FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AĄ;
                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           >269
193
215
>269
187
103
144
153
180
269
                                                                                                                                            (strain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16.9%;
28.0%;
                                                                                                                                                                                         Last sequence update)
Last annotation update)
SOLUBLE RECEPTOR PRECURSOR
                                                                                                                                                                                                                                                                Created)
                                                                                                                      on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43;
                                                                                                                      RNA
                                                                                                                                               Kasza)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 267; DB 1
Pred. No. 1e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TNFR-CYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TNFR-CYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TNFR-CYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYTOPLASMIC (POTENTIAL) 4 X TNFR-CYS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
CD40L RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-LINKED
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                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                      stage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   746903F30F95F387 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transmembrane;
                                                                                                                                          (SFV)
                                                                                                                                                                                                                                                                                                                  325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GLCNAC. . .)
                                                                                                                      Poxviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                  ΑA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Repeat; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                           (PROTEIN T2)
                                                                                                                    Chordopoxvirinae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14;
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MBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        117
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                         CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REPEAT
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00208; TNFR; 3.
PROSITE; PS00652; TNFR_NGFR_1; 2.
PROSITE; PS50050; TNFR_NGFR_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M17433; -; NOT_ANNOTATED_CDS. EMBL; A23727; CAA01687.1; -. PIR; B43692; B43692.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restricted the companies of the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-91207415; PubMed-1850261;
Smith C.A., Davis T., Wignall J.M., Din W.S., Farrah T., Upton
McFadden G., Goodwin R.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Upton C., Delange A.M., McFadden G.; "Tumorigenic poxviruses: genomic organization and DNA sequence of the telomeric region of the Shope fibroma virus genome."; Virology 160:20-30(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00020; TNFR_c6; 2. ProDom; PD000771; TNFR_c6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Receptor;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; P19438; 1TNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       form of the TNF receptor.";
  177
                                       180
                                                                             118
                                                                                                                    133
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                                                                                                                                                            60
                                                                                                                                                                                                    74
                                                                                                                                                                                                                                                                                 20 VLRLVLYLTFLGAPCYAPALP-----SCKEDEYPVGSECCPKCSPGYRVKEACGELTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANTIVIRAL EFFECTS OF THE CYTOKINE.
SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chem. Biophys. Res. Commun. 176:335-342 FUNCTION: BINDS TO TNF-ALPHA AND BETA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REACH CELLULAR TARGET AND THEREBY DEAMPENING
LYPVNETSCT---TTAG
                                                                             NGCRIC-APQTKCPAGYGVSGHTRAGDTLCEKCPPHTYSDSLSPTERCGTSFNYISVGFN
                                                                                                                    DHCAACRAYATSSPGQRVQKGGTESQDTLCQNCPPGTFSPN-GTLEEC------
                                                                                                                                                                                                    VCEPCPPGTYTAHLNGLSKCLQCQMCDPAMG-LRASRNCSRTENAVCGCSPGHFCIVQDG
                                                                                                                                                                                                                                            MLRLIALLVCV-VYVYGDDVPYSSNQGKCGGHDYEKDGLCCASCHPGFYASRLCGPGSNT
                                     ---QHQTKCSWLVTKAG
                                                                                                                                                            VCSPCEDGTFTASTNHAPACVSCR--GPCTGHLSESQPCDRTHDRVCNCSTGNYCLLKGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPR001368; TNFR_c6
                                                                                                                                                                                                                                                                                                                                                                                                                       17
27
27
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63
105
148
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238
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                                                                                                                                                                                                                                                                                                                                                                                                                       238 NW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            325
186
186
104
147
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186
105
105
                                                                                                                                                                                                                                                                                                                                            16.5%;
31.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COmmun. 176:335-342(1991).
TNF-ALPHA AND BETA. PROBABLY PREVENTS TNF
  190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Repeat; Signal.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                   TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR.
4 X TNPR-CYS.
TNPR-CYS 1.
TNPR-CYS 2.
TNPR-CYS 3.
TNPR-CYS 3.
TNPR-CYS 4.
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                         25;
                                                                                                                                                                                                                                                                                                                                         Score 260;
Pred. No.
                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                            0B 1;
4.5e-14;
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                                                                                                                                                                                                                                                                                                                                                          Length 325;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               THE
                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a collaboration -
                                                                                                                                                                                                                                                                                                                         30;
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ر
                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                            117
                                                                                                                                                                                                    132
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RESULT 6
TNR2_HUMAN

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TNR2_HUMAN
P20333;
01-FEB-1991
01-AUG-1991
20-AUG-2001
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20-AUG-2001 (Rel. 40, Last annotation update)
TUMOR NECROSIS FACTOR
BINDING PROTEIN 2) (TBPII) (P80) (TNF-R2) (P75) (CD120B) (ETANERCEPT).
TNFRSF1B OR TNFR2 OR TNFBR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kohno T., Brewer M.T., Baker S.L., Schwartz P.E., King M.W Hale K.K., Squires C.H., Thompson R.C., Vannice J.L.; "A second tumor necrosis factor receptor gene product can naturally occurring tumor necrosis factor inhibitor."; Proc. Natl. Acad. Sci. U.S.A. 87:8331-8335(1990).
MEDLINE-99221490;
Park Y.C., Burkit
                                                   Characterization of ligand phosphorylation.";
                                                                                  MEDLINE=93016040; PubMed=1328224; Pennica D., Lam V.T., Mize N.K., Lipari M.T., Goeddel D.V.;
                                                                                                         CHARACTERIZATION. MEDLINE-93016040;
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                                                                                                                                                                                             MEDLINE-91056048;
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                                                                                                                                                                                                                                        tumor necrosis
                                                                                                                                                                                                                                                "Two tumor necrosis factor-binding proteins purified from human urine. Evidence for immunological cross-reactivity with cell surface
                                                                                                                                                                                                                                                                        Engelmann
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                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 116-461
MEDLINE=90349572; Pu
Heller R.A., Song K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "A receptor for tumor necrosis factor cellular and viral proteins."; Science 248:1019-1023(1990).
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                     X-RAY CRYSTALLOGRAPHY
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Brockhaus M.;
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                                                                                                                                                                                                                                                                                                                                                                                                                   "Physical
                                                                         Biochemical properties of
                                                                                                                                                  Purification and partial amino acid sequence analysis of two listinct tumor necrosis factor receptors from HL60 cells.";
                                            Biol.
                                                                                                                                                                                                                                                                                                                             demonstration
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.A., Davis T., Anderson D.,
.K., Cosman D., Goodwin R.G
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                                                                                                                                                                                                                               Chem.
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                                                                                                                                        necrosis factor receptors 265:20131-20138(1990).
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265:1531-1536(1990)
                                                                                                                                                                                                                                                                                                                DNA cloning of a receptor for tumo; ion of a shed form of the receptor. ad. Sci. U.S.A. 87:6151-6155(1990).
                                         267:21172-21178(1992).
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; PubMed=2166946;
g K., Onasch M.A.,
PubMed=10206649;
t V., Villa A.R.,
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SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
DATABASE: NAME-PROW; NOTE-CD guide CD120b entry;
WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cd120b.htm".
DATABASE: NAME-Enbrel; NOTE-Clinical information on Enbrel;
WWW-"http://www.enbrelinfo.com/".
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APPROXIMATELY 5-FOLD LOWER AFFILING THE BETA.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
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ProDom; PD000771; TNFR_c6; 1. SMART; SM00208; TNFR; 4. L; U52162; AAC50622.1 L; U52163; AAC50622.1 L; U52164; AAC50622.1 L; M55994; AAA36755.1 ; A35356; A35356. "IPR001368; TNFR_c6 Transmembrane; 12-APR-99 A36007. A36475. AAC50622. AAC50622. AAA59929. AAA63262. TNFR_c6; pharmaceutical; 3D-st TNFR_NGFR_2; 4. TNFR_NGFR_1; 461 257 287 287 201 201 118 118 201 53 201 53 118 118 118 JOINED.
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HSSP; P19438; INCF.
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Pfam; PF00020; TNFR_c6; 2.
ProDom; PD000771; TNFR_c6; 1.
SMART; SM00208; TNFR; 2.
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STRAIN-INDIA-1967 / ISOLATE IND3;
MEDLINE-93202281; PubMed=8384129;
Shchelkunov S.N., Blinov V.M., Sandakhchiev L.S.;
"Genes of variola and vaccinia viruses necessary to overcome the he protective mechanisms.";
FEBS Lett. 319:80-83(1993).
-i- SIMILARITY: CONTAINS 2 LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGIONS.
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01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
PROTEIN C22/B28 HOMOLOG.
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EMBL; X67117; CAA47540.1;
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                                                                                            use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                   Crowe P.D., van Arsdale T.L., Walter B.N., Ware C.F., Hession C., Ehrenfels B., Browning J.L., Din W.S., Goodwin R.G., Smith C.A.; "A lymphotoxin-beta-specific receptor."; Science 264:707-710(1994).

-i- FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION
                                                                                                                                                                                                                                                                                                                                                                      Baens M., Chaffanet M., Cassiman J.J., den Berghe H., Marynen "Construction and evaluation of a hncDNA library of human 12p transcribed sequences derived from a somatic cell hybrid."; Genomics 16:214-218(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P36941;
01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1994 (Rel. 29, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
LYMPHOTOXIN-BETA RECEPTOR PRECURSOR (TUMOR NECROSIS FACTOR
2 RELATED PROTEIN) (TUMOR NECROSIS FACTOR C RECEPTOR).
          InterPro; IPR0
Pfam; PF00020;
                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Liver;
MEDLINE=93252381; PubMed=8486360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LTBR OR TNFCR OR TNFRSF3. Homo sapiens (Human).
                                                                                                                                                     the European Bioinformatics Institute.

    -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
    -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION

                                                                                                                                                                                                                                                                                                                              MEDLINE=94225209; PubMed=8171323;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TNRC_HUMAN
                                                                                                                                                                                                                                                                                                                                                FUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 LRLVLYLTFLGAPC-----YAPALPSCKEDEYPVGSECCPKCSPGYRVKEACGEL
                                                                                                                                                                                                                                             IMMUNE
                                                                                                                                                                  SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YIDVEITLYPVNDTSCTRTTT---TGLSES----ILTSELTITM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MKSVLYLYILFLSCIIINGRDAAPYTPPNGKCKDTEYKRHNLCCLSCPPGTYASRLCDSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ECQ------HOTKCSWLVTKAGAGTSSSHWVWWFLSGSLVIVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QDGDHCAACRAYATSSPGQRVQKGGTESQDTLCQNCPPGTFS------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     THTQCTPCGSGTFTSRNNHLPACLSCNGRCN--SNQVETRSCHTTHNRICECSPGYYCLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGTVCEPCPPGTYIAHLNGLSKCLQCQ-MCDPAMGLRASRNCSRTENAVCGCSPGHFCIV 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KGSSGCKACVSQTKCGIGYGV-SGHTSVGDVICSPCGFGTYSHTVSSADKCEPVPNNTFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eutheria;
                      IPR001368; TNFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          349
                                                                                                                                                                                                                                            DEVELOPMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                    AAA36757
        TNFR_c6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16.3%;
29.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 257; DB 1;
Pred. No. 8.4e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TNFR-CYS 2.
D45D40B5C6E780EF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Ve
Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  435
                                                                                                                                                   There are no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vertebrata; Euteleostomi; ; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ₽
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                                                                                                           Usage by and for http://www.isb-sib.
                                                                                                                                       its content
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CRC64;
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                                                                                                                                                     restrictions
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                                                                                                                                                                    collaboration
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Best Local S
Matches 86
                                                  01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence up
01-NOV-1997 (Rel. 35, Last annotation
LYMPHOTOXIN-BETA RECEPTOR PRECURSOR.
LIBR OR THECR.
Mus muschin-
                                                                                                            TNRC_MOUSE
P50284;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REPEAT
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
DOMAIN
REPEAT
SEQUENCE FROM N.A
                Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00208; TNFR; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Receptor;
                                                                                                                                                                                                                                                         171
                                                                                                                                                                                                                                                                             166
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                                                                                                                                                                                              262
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                       4
                                                 musculus
                                                                                                                                                                                            -- PDVTTVAVEETIPSFTGRSP
                                                                                                                                                                                                                                                         KAGHFQNTSSPSA----RCQPHTRCENQGLVEAAPGTAQSDTTCKNPLEPLPPEMSGTMLM
                                                                                                                                                                        YFPDL----VQPLLPISGDVSP
                                                                                                                                                                                                                                  VIVCSTVGLII------CVKRRKPRGDVVKVIVSVQRKRQEAEGEATVIEALQAP----
                                                                                                                       MOUSE
                                                                                                                                                                                                                 LAVLLPLAFFLLLATVFSCIWKSHP--SLCRKLGSLLKRRPQGEGPNPVAGSWEPPKAHP
                                                                                                                                                                                                                                                                                                TSKRKTQCRCQPGMFCAAW-ALECTHCELLSDCPPGTEAELKDEVGKGNNH-----CVPC
                                                                                                                                                                                                                                                                                                                    SRTENAVCGCSPGHFCIVQDGDHCAACRAYATSSPG-----QRVQKGGTESQDTLCQNC
                                                                                                                                                                                                                                                                                                                                                                                                     PG-DWGPPPWRSTPRTDVLRLVLYLTFL-----GAPCYAPALPSCK--EDEY--PVGS
                                                                                                                                                                                                                                                                                                                                        ICCSRCPPGTYVSAKCSRIRDTVCATCAENSYNEHWNYLTICQLCRPCDPVMGLEEIAPC
                                                                                                                                                                                                                                                                                                                                                              ECCPKCSPGYRVKEACGELTGTVCEPCPPGTYIAHLNGLSKCLQCQMCDPAMGLRASRNC
                                                                                                                                                                                                                                                                                                                                                                                  PGLAWGP----
                                                                                                                                                                                                                                                                                                                                                                                                                           86;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        228
249
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125
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1101
1104
1126
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1170
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                                                (Mouse)
                                                                                                                                                                                                                                                                          SPNGTLEECQHQTKC-SWLVTKAGAGTSSSHWVWW-----FLSGSLVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA;
                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TNFR_NGFR_1; 2.
TNFR_NGFR_2; 3.
                           Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46709
                                                                                                                                                                                                                                                                                                                                                                                 -----LVLGLFGLLAASQPQAVPPYASENQTCRDQEKEYYEPQHR
                                                                                                                                                                                                                                                                                                                                                                                                                                   16.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glycoprotein; Repeat; Signal.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Œ,
                                                                                                                                                                                                                                                                                                                                                                                                                         ; Score 253; DB 1;
; Pred. No. 2.2e-13;
37; Mismatches 127
                                                                                                                                                                         303
                                                                                                                                                                                             281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 X TNFR-CYS.
TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BY SIMILA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LYMPHOTOXIN-BETA RECEPTOR EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TNFR-CYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC (POTENTIAL)
                           Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -LINKED (GLCNAC. . .) (P-LINKED (GLCNAC. . .) (P-LINKED (GLCNAC. . .) (P624626E6022F656F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Y SIMILARITY.
                                                                                         update)
                                                                                                                       415 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4
                                                                              update)
                                                                                                                                                                                                                                                                                                                                                                                                                          127;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 435;
                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                              Mus
                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Best Local S
Matches 83
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Prodom; Purch
CMART; SM00208; 1
                                                                                                                                                                                 REPEAT
DISULFID
                                                                                                                                                   CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
REPEAT
REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00652; THER_NGFR_1; PS50050; THER_NGFR_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             modified and this statement is not removentities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence trap and chromosomal mapping Genomics 30:312-319(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00020; TNFR_c6; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MGD; MGI:104875;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U29173; AAA68964.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PRC-!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nakamura T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and expression."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Force W.R., Walter B.N., Hession Browning J.L., Ware C.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=CVB; TISSUE=Lung;
MEDLINE=96072804; PubMed=7594541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The murine lymphotoxin-beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Honjo T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=96163885;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Mouse lymphotoxin-beta receptor.
 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IMMUNE DEVELOPMENT
 WGPLLLGLSGLLVASQPQLVPPYRIENQT-
                                 WGP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              L38423; AAB00846.1;
U30798; AAA81334.1;
                                                                . Similarity 25. 83; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PD000771; TNFR_c6; M00208; TNFR; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                non-profit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transmembrane;
                                                                                                                                              179
415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        155:5280-5288(1995).
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                                                                                                                                                   AA;
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415
223
244
                                                                                                                                                                                    170
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213
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80
98
116
1124
132
150
169
187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 institutions as long as its content tatement is not removed. Usage by a
                                                                                                                                                   44956
                                                                                15.6%;
                               -PPWRSTPRTDVLRLVLYLTFLGAPCYAPALPSCKEDEY--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nazarea M.,
                                                                                                                                                   ₩,
                                                                                                                                              TNFR-CYS 4.

BY SIMILARITY.

O-LINKED (GLCNAC. . .) (POTO 10 No. 11 
                                                                  40;
                                                                Score 245.5; DB 1;
Pred. No. 8.3e-13;
0; Mismatches 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      receptor cDNA:
                                                                                                                                                                                                                                                                                                                                                                                                                   4 X TNFR-CYS.
TNFR-CYS 1.
                                                                                                                                                                                                                                                                                                                                                                                       TNFR-CYS
                                                                                                                                                                                                                                                                                                                                                                                                       TNFR-CYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EXTRACELLULAR
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OX40_RAT
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TRANSMEM
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SIGNAL
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P15725;
                                                                                                                                   CHAIN
                                                                                                                                                                                                                                                                      ProDom; PD000771; TNFR_c6; 1. SMART; SM00208; TNFR; 3.
                                                                                                                                                                                                                                                                                                                        InterPro; IPR001368; TNFR_c6.
Pfam; PF00020; TNFR_c6; 3.
                                                                                                                                                                                                                                                                                                                                                                    PIR; S08036; S08036.
PIR; S12783; S12783.
HSSP; P25942; 1CDF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Characterization of the MRC OX40 antigen of activated CD4 positive." The MRC OX40 antigen of activated CD4 positive. Tymphocytes -- a molecule related to nerve growth factor receptor."; EMBO J. 9:1063-1068(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TNFRSF4 OR TXGP1L OR OX40.
Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
0X40L RECEPTOR PRECURSOR (OX40 ANTIGEN) (MRC
                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X17037; CAA34897.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-90214614; PubMed-2157591;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
TISSUE SPECIFICITY: ACTIVATED T-CELLS.
SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PHFPDLA-EPLLPMSGDLSPS
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requires a license agreement (See
an email to license@isb-sib.ch).
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                                                                                                                                                                                                 TNFR_NGFR_1; 3.
TNFR_NGFR_2; 2.
Antigen; Glycoprotein; Transmembrane; Repeat;
19
271
210
235
235
271
164
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                                                        POTENTIAL.
CYTOPLASMIC (POTENTIAL)
                                                                                                        OX40L RECEPTOR.

EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
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                                       TNFR-CYS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (See http://www.isb-sib.ch/announce/
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Best Local S
Matches 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VT2_MYXVL
P29825;
                                                                                                                   EMBL; M95181; AAA46632.1; -.
EMBL; A23729; CAA01688.1; -.
PIR; A40566; GQVZML.
HSSP; P19438; 1TNR.
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CARBOHYD
                                            PROSITE; PS00652; TNFR_NGFR_1; 2. PROSITE; PS50050; TNFR_NGFR_2; 2.
                                                                    Pfam; PF00020; TNFR_c6; 2. ProDom; PD000771; TNFR_c6; 1. SMART; SM00208; TNFR; 3.
                                                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Extremena Bioinformatics Institute. There are no restruce by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                    Upton C., Macen J.L., Schreiber M., McFadden G.; "Myxoma virus expresses a secreted protein with homology necrosis factor receptor gene family that contributes to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR PRECURSOR
                                                                                                         InterPro; IPR001368; TNFR_c6
                                                                                                                                                                                                         modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                  Virology 184:370-382(1991).
                                                                                                                                                                                                                                                                                                                                           virulence.";
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Viruses; dsDNA viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Myxoma virus (strain Lausanne)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REPEAT
REPEAT
REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25
                                                                                                                                                                                                                                                                             ANTIVIRAL EFFECTS OF THE CYTOKINE. SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
                                                                                                                                                                                                                                                                                                        REACH CELLULAR TARGET AND THEREBY DEAMPENING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HRSGSELKQNCTPTEDTVCQCRPG-TQPRQDSSH---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LCQNCPPGTFSPNGTLEECQHQTKCS 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCVKDTYPSGHKCCRECQPGHGMVSRCDHTRDTVCHPCEPGFYNEAVN-YDTCKQCTQCN 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PAMGLRASRNCSRTENAVCGCSPGHFCIVQDGDHCAACRAYATSSPGQRVQKGGTESQDT 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -CVPCPPGHFSP-GSNQACKPWINCI 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              l Similarity
51; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         271 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25
61
103
124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  102
123
143
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TNER-CYS 3 (INCOMPLETE).
TNER-CYS 4.
TNER-CYS 4.
N-LINKED (GLONATING)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       RNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 240.5; DB 1;
Pred. No. 1.4e-12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     stage;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    326
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A
                                                                                                                                                                                                                                                                                                                   PROBABLY PREVENTS INF
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                                                                                                                                                                                                         Usage
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                                                                                                                                                                                                                                restrictions
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SIGNAL CHAIN DOMAIN

1 17 27

POTENTIAL.
TUMOR NECROSIS
4 X TNFR-CYS.

FACTOR

SOLUBLE

Receptor;

Glycoprotein; Repeat; Signal.

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FASA_PIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 73
                                                                                    myocardium of pig. ";

Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.

FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASL. THE ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION. ACTIVE CASPASE-8 INITLATES THE SUBSEQUENT CASCADE CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING APOPTOSIS. FAS-MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED SUICIDE OF MATURE T-CELLS, OR BOTH (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
             This
                                                                                                                                                                                                                                                                                                                                  FASL RECEPTOR PRECURSOR (APO-1 ANTIGEN) (CD95).
TNFRSF6 OR APT1 OR FAS.
Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                       077736;
15-JUL-1999 (Rel. 38,
15-JUL-1999 (Rel. 38,
20-AUG-2001 (Rel. 40,
                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammaila; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REPEAT
REPEAT
                                                    <del>-</del>
                                                                                                                                                                                                                                                          Bartling
                                                                                                                                                                                                                                                                                                NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                           FASA_PIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REPEAT
                                                                                                                                                                                                                                         Bartling B., Hoffmann J., Holtz J.,
Expression of apoptosis-associated
Bartling of pig ".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REPEAT
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                                     SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE SIMILARITY: CONTAINS 1 DEATH DOMAIN.
                                                               DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                          UL-1999 (Rel. 38, Last sequence update)
UG-2001 (Rel. 40, Last annotation update)
RECEPTOR PRECURSOR (APOPTOSIS-MEDIATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DRYQNTTKMCTLNIEIRCVE----GDAVRTI 260
            SWISS-PROT entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----HQTKCSWLVTKAGA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EGCRIC-APKTKCPAGYGVSGHTRTGDVLCTKCPRYTYSDAVSSTETCTSSFNYISVEFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DHCAACRAYATSSPGQRVQKGGTESQDTLCQNCPPGTFSPN-GTLEECQ-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VCEPCPPGTYIAHLNGLSKCLQCQ-MCDPAMGLRASRNCSRTENAVCGCSPGHFCIVQDG 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MFRLTLLLAYVACVYGGGAP-YGADRGKCRGNDYEKDGLCCTSCPPGSYASRLCGPGSDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LYPVNDTSCT----TTAGPNEVVKTSEFSVTLNHTDCDPVFHTEYYGTSGSEGAGGFFTGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VCSPCKNETFTASTNHAPACVSCRGRC--TGHLSESQSCDKTRDRVCDCSAGNYCLLKGQ
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73; Conserv
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  the
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 Swiss Institute
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26.8%;
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is copyright. It is produced through a collaboration stitute of Bioinformatics and the EMBL outstation -
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Pred. No. 2.4e-
30; Mismatches
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N-LINKED
N-LINKED
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TNFR-CYS
TNFR-CYS
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N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
ABBF027E947292FF C
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e-12;
104;
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                                                   CYSTEINE-RICH REGION
                                                                                                                                                                                                                                                                                                                                                                             SURFACE
                                                                                                                                                                                                                                                          Heusch G.,
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(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                                                             Euteleostomi;
Sus.
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                                                                                                                                                                                                                                                                                                                                                                             FAS)
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                           OX40_MOUSE STANDARI
P47741;
01-FEB-1996 (Rel. 33, 0
01-FEB-1996 (Rel. 33, 1
20-AUG-2001 (Rel. 40, 1
                                                                                                              20-AUG-2001 (Rel. 33, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
0X401 RECEPTOR PRECURSOR (OX40 ANTIGEN).
TNERSF4 OR TXGP1 OR OX40.
                                                                                                                                                                                                    MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
CARBOHYD
SEQUENCE FROM N.A.
STRAIN-BALB/C;
MEDLINE-94044750; PubMed-8228223;
Calderhead D.M., Buhlmann J.E., v
Claassen E., Noelle R.J., Fell H.
"Cloning of mouse Ox40: a T cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REPEAT
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00005; DEATH; 1.
SMART; SM00208; TNFR; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed
                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00531; death; 1 Pfam; PF00020; TNFR_c6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an
                                                                             NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHAIN
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                                                                                                                                                                                                                                                                     TYGLIICYKRRKPRGDYYKVIYSYQRKRQEAEGEATVIEALQAPPDYTTYAVEETI 273
                                                                                                                                                                                                                                                 LVYREVKRRCRRKENGYQKPITS-----NAE-EVPMIKDVDLGKYITRIAEQMKI
                                                                                                                                                                                                                                                                                                         TLCQNCPPGTFSPNGTLEEC--QHQTKCSWLVTKAGAGTSSSHWVWWFLSGSLVIVIVCS
                                                                                                                                                                                                                                                                                                                                                                                CPEGQHREGQFCCQPCPPGKRKHADCTSPGGAPQCVPCSEGEDYTDKNHHSSKCRRCRVC 105
                                                                                                                                                                                                                                                                                                                                                                                               CKEDEYPVGSECCPKCSPGYRVKEACGELTGT-VCEPCPPG-TYIAHLNGLSKCLQCQMC
                                                                                                                                                                                                                                                                                                                                      DGEHGLEVEKNCTRTQNTKCRCKPNFFCHTSQCEHCNPC
                                                                                                                                                                                                                                                                                                                                                           DPAMGLRASRNCSRTENAVCGCSPGHFCIVQDGDHCAACRAYATSSPGQRVQKGGTESQD
                                                                                                                                                                                                                                                                                                                                                                                                                              65;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PS50050; TNFR_NGFR_2; 2. PS50017; DEATH_DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PS00652; TNFR_NGFR_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR000488; Death.
IPR001368; TNFR_c6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   332
                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a license agreement
                                                                                                                                                                                                                                                                                            HGVIENCTPTSNTKCREVFQSAGS-RSNLHWLW
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175
192
332
364
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125
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1311
                                                                                         Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                       15.0%;
27.5%;
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                                                                                                                                                                     Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                            30;
                                                                                                                                                                                                                                                                                                                                                                                                                           Score 236; DB
Pred. No. 3.9e
80; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 X TNFR-CYS.
TNFR-CYS 1.
TNFR-CYS 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-LINKED (GLCNAC. . N-LINKED (GLCNAC. .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TNFR-CYS
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3 X TNFR-CYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEATH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EXTRACELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FASL RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL
                                                                                        Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5B8B03682756BF1B
                       van
  activation marker that may mediate
                       den
                                                                                                                                                                                            272
                                                                                                                                               update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  There are no rest
                       Eertwegh A.J.,
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SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Gene structure and chromosomal localization of rat OX40 protein.";
Eur. J. Immunol. 25:926-930(1995).
-!- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CY7
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Birkeland M.L., Copeland N.G., Gilbert D.J., Jenkins N.A.
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SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION
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[mmunol. 151:5261-5271(1993).
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PS50050; THER_NGFR_2; 2.
PS50050; THER_NGFR_2; 2.
   (Rel. 22, Created)
(Rel. 22, Last sequence update)
(Rel. 38, Last annotation update)
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TNFR-CYS 3 (INCOMPLETE).
TNFR-CYS 4.
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EMBL; M60469; AAA39752.1; -
EMBL; M59378; AAA40463.1; -
EMBL; M59378; CAA65021.1; -
EMBL; X87128; CAA60618.1; -
PIR; B38634; B38634.
                                                                                                                                                                                                                                                                                                                       MGD; MGI:1314883; Tnfrsflb.
InterPro; IPR001368; TNFR_c6.
Pfam; PF00020; TNFR_c6; 4.
ProDom; PD000771; TNFR_c6; 1.
SMART; SM00208; TNFR; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isborsend an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-91246168; PubMed-1645445;
Goodwin R.G., Anderson D., Jerzy R., Dav
Copeland N.G., Jenkins N.A., Smith C.A.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Molecular cloning and expression of the type 1 and type 2 murine receptors for tumor necrosis factor.";
Mol. Cell. Biol. 11:3020-3026(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;

    -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
    -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.

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TNFR_NGFR_2;
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Rodentia;
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., Goeddel D.V
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                                                                                                     Biochem. Biophys. Res. Commun. 198:666-674(1994).

-:- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASL. THE ADAPTOR MOLECULE FADD RECRUITS CASSPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEDLYTIC ACTIVATION. ACTIVE CASPASE-8 INITIATES THE SUBSEQUENT CASCADE OF CASPASES (ASPARTAME-SPECIFIC CYSTEINE PROTEASES) MEDIATING APOPTOSIS. FAS-MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF PERLIPHERAL TOLERANCE, IN THE ANTIGEM-STIMULATED SUICIDE OF MATURE T-CELLS, OR BOTH (BY SIMILARITY).

-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-!- SUBCELLULAR CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD, AND MAXEE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.

-!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                  Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
FASL RECEPTOR PRECURSOR (APOPTOSIS-MEDIATING
(APO-1 ANTIGEN) (CD95).
TNERSF6 OR PTI OR FAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10116;
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Mammalia; Eutheria; Rodentia;
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                  SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                          rat liver.";
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55; Conser
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BY GLCNAC. . .) (POT N-LINKED (GLCNAC. . .) (POT M-LINKED (GLCN
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Pred. No. 3.5e-10;
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Sciurognathi; Muridae;
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SEQUENCE
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DOMAIN
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Pfam; PF00020; TNFR_C6; 3.
SMART; SM00005; DEATH; 1.
SMART; SM00208; TNFR; 3.
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                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00652; TNFR_NGFR_1; PROSITE; PS50050; TNFR_NGFR_2; PROSITE; PS50017; DEATH_DOMAIN;
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                   VGLIICVKRRKPRGDVVKVIVSVQRKRQEAEGEATVIEALQAPPDVTTVAVEETI
                                         NTKCKK---
                                                             DTLCQNCPPGTFSPNGTLEECQHQTKCSWLVTKAGAGTSSSHWVWWFLSGSLVIVIVCST
                                                                                  CDEGHGLEVETNCTRTQNTKCRCKENFYCNASLCDHCYHC----TSCGLEDILEPCTRTS 158
                                                                                               CDPAMGLRASRNCSRTENAVCGCSPGHFCIVQDGDHCAACRAYATSSPGQRVQKGGTESQ 158
                                                                                                                          NCSEGLYQVGPFCCQPCQPGERKVKDCTTSGGAPTCHPCTEGEEYTDRKHYSDKCRRCAF 102
                                                                                                                                              SCKEDEYPVGSECCPKCSPGYRVKEACGELTGT-VCEPCPPG-TYIAHLNGLSKCLQCQM 98
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58; Conser
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21 BY SIMILARITY.
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-YRKRQPGDPESGIPSPESVPMNVSDVNLNKYI 222
                                                                                                                                                                                                                                                                        TNFR-CYS
                                                                                                                                                                                                                              N-LINKED
                                                                                                                                                                  Score 206.5; DB 1
Pred. No. 9.1e-10;
7; Mismatches 93
                                                                                                                                                                                                                                                   N-LINKED
                                                                                                                                                                                                                                                               DEATH.
                                                                                                                                                                                                                                                                                            TNFR-CYS
                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL).
3 X TNFR-CYS.
                                                                                                                                                                                                                                                                                                                             POTENTIAL.
                                                                                                                                                                                                                                                                                                                                      EXTRACELLULAR (POTENTIAL).
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N-LINKED (GLCNAC. .
N-LINKED (GLCNAC. .
D25D583C909D9D09 C1
                                        -----QSSNYKLLWLL-----ILPGL
                                                                                                                                                                                                                                                                         ω N F
                                                                                                                                                                                     DB 1;
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                                                                                                                                                                    93;
                                                                                                                                                                                                                      CRC64;
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                                                                                                                                                                                                                              ) (POTENTIAL).
) (POTENTIAL).
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Search completed: January 24, 2002, 16:25:16 Job time: 191 sec

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd. خا

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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3: sp_fungi:*
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Gapop 10.0 , Gapext 0.5
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sp_vertebrate:*
sp_unclassified:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO. 1 1 2 3 4 5 5 6 6 7	Score 1303.5 271.5 269.5 269.5 269.5 269.5
ω 4	269.5 269.5
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7 6	269.5 269.5
8	268.5
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12	265.5
13	265.5
14	265
15	262.5
16	262
17	259
18	257.5
19	257 5

DP PP

Query Match 82.6 Best Local Similarity 82.0 Matches 232; Conservative

82.6%; Score 1303.5; DB 6; Length 283;. 82.0%; Pred. No. 4.4e-116; Live 18; Mismatches 30; Indels 3;

Gaps

2

	44						38							31		29	28					23	22	21	20
218	219.5	219.5	225.5	225.5	226.5	227	228	228	228.5	229	229.5	232.5	236.5	239	243.5	246	249	249.5	251.5	254.5	254.5	257	257	257	257.5
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ALIGNMENTS

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Pfam; PF00020; TNFR_c6; 2.
ProDom; pD000771; TNFR_c6; 1.
SMART; SM00208; TNFR; 2.
PR0SITE; PS000652; TNFR_NGFR_1; 2
PR0SITE; PS000650; TNFR_NGFR_2; 2
SEQUENCE 349 AA; 38239 MW; D)
        057277
057277;
01-JUN-1998
01-JUN-1998
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057100;
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01-JUN-1998
01-JUN-2001
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Loparev V.N., Parsons J.M., Esposito J.J.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases
EMBL; U87844; AAB94361.1; -.
HSSP; P25942; ICDF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Viruses; dsDNA viruses, Orthopoxvirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Monkeypox virus.
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                                                                                                          T 173
                                                                                                                                                                                                                                                                                 LRLVLYLTFLGAPC-----YAPALPSCKEDEYPVGSECCPKCSPGYRVKEACGEL 70
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                                                                                                                                                                                                       THTOCTPCGSDTFTSHNNHLQACLSCNGRCD--SNQVETRSCNTTHNRLCECSPGYYCLL 118
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                                                                                                                                                                                                                               TGTVCEPCPPGTYIAHLNGLSKCLQCQ-MCDPAMGLRASRNCSRTENAVCGCSPGHFCIV 129
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          (TrEMBLrel.
                                                                                                                                                                                                                                                                                                         Conservative
                                             PRELIMINARY;
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          Last sequence update)
                     Created)
                                                                                                                                                                                                                                                                                                        Score 271.5; I
Pred. No. 7.6e
23; Mismatches
                                             PRT;
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2.
DF6C280D478F2422 CRC64;
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les 80;
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Query Match 17.1%; S
Best Local Similarity 32.6%; P
Matches 57; Conservative 25;
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Best Local Similarity
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Pfam; PF00020; TNFR_c6; 2.

ProDom; DP000071; TNFR; c6; 1.

SMART; SM00208; TNFR; 2.

PROSITE; PS00652; TNFR_NGFR_1; 2.

PROSITE; PS50050; TNFR_NGFR_2; 2.

SEQUENCE 348 AA; 38212 MW; 5.
                                                                                                                                                                                                                                                                                                                                                                             057108; PRELIMINARY; PRT; 348 AA. 057108; O1-JUN-1998 (TrEMBLrel 06, Created) 01-JUN-1998 (TrEMBLrel 06, Last sequence update) 01-JUN-2001 (TrEMBLrel 17, Last annotation update)
                                                                      Interpro; IPR001368; TNFR_c6.

Pfam; PF00020; TNFR_c6; 2.

ProDom; PD000771; TNFR_c6; 1.

SMART; SM00208; TNFF; 2.

PROSITE; PS00652; TNFR_NGFR_1; 2.

PROSITE; PS50050; TNFR_NGFR_2; 2.

PROSITE; PS50050; TNFR_NGFR_2; 2.
                                                                                                                                                                                                                 Loparev V.N., Parsons J.M., Submitted (FEB-1997) to the
                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-ZAIRE-1970 (CONGO-8);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-ZAIRE-1996(96-17), ZAIRE-1996 (96-16);
STRAIN-ZAIRE-1996(96-17), ESPOSITO J.J.;
LOPAIROW V.N., PAISONS J.M., ESPOSITO J.J.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ
EMBL; U88543; AAB94378.1; -.
EMBL; U87841; AAB94378.1; -.
EMBL; U87841; AAB94358.1; -.
HSSP; P25942; ICDF.
                                                                                                                                                                                  EMBL; U88142; AAB94367.1; -. HSSP; P25942; ICDF.
                                                                                                                                                                                                                                                                                           NCBI_TaxID=10244;
                                                                                                                                                                                                                                                                                                           Orthopoxvirus:
                                                                                                                                                                                                                                                                                                                        Viruses; dsDNA viruses,
                                                                                                                                                                                                                                                                                                                                          Monkeypox virus
                                                                                                                                                                                                                                                                                                                                                                       TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2001 (TrEMBLrel. 17, Last annotation update) TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGTVCEPCPPGTYIAHLNGLSKCLQCQ-MCDPAMGLRASRNCSRTENAVCGCSPGHFCIV 129
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                                                                                                                                                                                                                 Esposito J.J.;
EMBL/GenBank/DDBJ
Score 269.5; DB 1
Pred. No. 1.2e-17;
5; Mismatches 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 269.5; DB 12; Pred. No. 1.2e-17;
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2.
54019521556C2D8F CRC64;
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                            DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78;
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Best Local S
Matches 59
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Pfam; PF00020; TNFR_c6; 2.
ProDom; PD000771; TNFR_c6; 1.
SMART; SM00208; TNFR; 2.
PR0SITE; PS00052; TNFR_NGFR_1; 2
PR0SITE; PS50050; TNFR_NGFR_2; 2
SEQUENCE 349 AA; 38295 MW; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Loparev V.N., Parsons J.M., Es
Submitted (JAN-1998) to the EM
EMBL; U88144; AAB94369.1; -
EMBL; U87842; AAB94359.1; -
EMBL; U87994; AAB94365.1; -
EMBL; U87995; AAB94366.1; -
EMBL; U88143; AAB94368.1; -
EMBL; U88143; AAB94368.1; -
057101;
057101;
01-JUN-1998
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les 59; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                        KGASGCRTCISKTKCGIGYGV-SGYTSTGDVICSPCGPGTYS-----HTVSSTDKCEPVV 172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGTVCEPCPPGTYIAHLNGLSKCLQCQ-MCDPAMGLRASRNCSRTENAVCGCSPGHFCIV 129
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       (TrEMBLrel. 06,
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                                                                        PRELIMINARY;
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       Created)
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CBD2C949ED2B8E7C CRC64;
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Loparev V.N., Parsons J.M., Esposito J.J.;

Loubmitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.

EMBL; U87845; AAB94362.1; -.

RESSP; P25942; 1CDE.

RISSP; P25942; 1CDE.

RISSP; P25942; 1CDE.

RISSP; P25020; TNFR_C6; 2.

R Pfam; PF00020; TNFR_C6; 1.

R ProDom; PD000771; TNFR_C6; 1.

R PROSITE; PS0052; TNFR_NGFR_1; 2.

R PROSITE; PS00552; TNFR_NGFR_2; 2.

SEQUENCE. 349 AA; 38311 MW; 02F65B00CFB858BE CRC64;
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Best Local Similarity
Matches 59; Conser
                            InterPro; IPRO01368; TNFR_c6.
Pfam; PF00020; TNFR_c6; 2.
ProDom; pD000771; TNFR_c6; 1.
SMART; SM00208; TNFR; 2.
PROSITE; PS00652; TNFR_NGFR_1; 2
PROSITE; PS500650; TNFR_NGFR_2; 2
SEQUENCE 349 AA; 38308 MW; C.
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057102;
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation updat
TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-BENIN-1978 (78-3945);
LOPAREV V.N., PAISONS J.M., ESPOSITO J.J.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases
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HSSP; P25942; 1CDF
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NCBI_TaxID=10244;
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Pred. No. 1.2e
22; Mismatches
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2;
CBD2C949F994C59C CRC64;
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1.2e-17;

81;

Indels Length 349;

19;

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5

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DB 12;

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RESULT
Q99NE2
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Q99NE1
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Matches 59
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       Q99NE2;
Q99NE2;
01-JUN-2001
01-JUN-2001
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Tone M., Tone Y., Fairchild P.J., Wykes M., Wald "Regulation of CD40 function by its isoforms gen aiternative spilicing.";
Proc. Natl. Acad. Sci. U.S.A. 98:1751-1756(2001) EMBL; AJ401389; CAC29499 MW; EE21E6C76FB4ZDEF
                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Rodentia;
NCBI_TaxID=10090;
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01-JUN-2001 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
CD40 TYPE IV ISOFORM.
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                                                                                                                     VCHPCPVGFFSNQSSLFEKCYPWTSCEDKNLEVLQK--
                                                                                                                                        LCQNCPPGTFSPNGTL-EECQHQTKCS----WLVTKAGAGTSSSHWVWWFLSGSLVIVIV 215
                                                                                                                                                          PNQGLRVKKEGTAESDTVCTCKEGQHCTSKD---CEACAQHTPCIPGFGVMEMATETTDT
                                                                                                                                                                            PAMGLRASRNCSRTENAVCGCSPGHFCIVQDGDHCAACRAYATSSPGQRVQKGGTESQDT 160
                                                                                                                                                                                              TCSDKQYLHDGQCCDLCQPGSRLTSHCTALEKTQCHPCDSGEFSAQWNREIRCHQHRHCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MRSVLYSYILFLSCIIINGRDIAPHAPSNGKCKDNEYRSRNLCCLSCPPGTYASRLCDSK 60
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59; Conser
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       (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                  208
                                                                                                                                                                                                                                           17.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17.1%;
32.6%;
        17,
17,
                                                                                                                                                                                                                                                                                                                                                                                                                         17,
17,
17,
                                                                                                                                                                                                                                  32;
                Created)
        Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                           Score 268.5;
Pred. No. 9e-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 269.5; DB 12;
Pred. No. 1.2e-17;
2; Mismatches 81;
                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                EE21E6C76FB42DEF CRC64;
                                                                                                                                                                                                                                    Mismatches
                                    234
                                                                                                                                                                                                                                                                                                                                                                                                                                                               222
                                                                                                                                                                                                                                           9e-18;
                                    AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                               A
                                                                                                                                                                                                                                                                                                                                                                                                                                   update)
                                                                                                                                                                                                                                                    DB 11;
                                                                                                                      -GTSQTNVICGLKSRMRALLVI 198
                                                                                                                                                                                                                                                                                                                   Waldmann H
s generated
                                                                                                                                                                                                                                                                                                                                                                                                                        update)
                                                                                                                                                                                                                                   ; 68
                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                    through
                                                                                                                                                                                                                                                     222;
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                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                          141
                                                                                                                                                                                               84
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                                                               В
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                                                                                                                                                                                                                                                                                                                                                                                    Дβ
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                                                                                                                                                                                                                                                                                                                                                                                                                          В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Loc
Matches
                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                              Camelpox virus (strain CP-1).
Viruses, dsDNA viruses, no RN
Orthopoxvirus.
                                                                                                                                                                                                                                            CRMB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CD40.
                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                      NCBI_TaxID=28873;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2001 (TrEMBLrel. CD40 TYPE III ISOFORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                 199
                                                                                                                                                                                                                                                                                                                                                                 216
                                                                                                                                                                                                                                                                                                                                                                                    142
                                                                                                                                                                                                                                                                                                                                                                                                      161
                                                                                                                                                                                                                                                                                                                                                                                                                                           101
                Local Similarity hes 57; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                          85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                              25
                                                                                                                                                                                                                                                                                                                    10
                                                                                                                                                                                                                                                                                                                                                 PVVMGILITI
                                                                                                                                                                                                                                                                                                                                                                 CSTYGLIICY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                234 AA;
                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                 208
                                                                                                                                                                                                                                                                                                                                                                 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25747 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17.0%;
                         16.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32;
                                                                                                                                                                                                                          RNA
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STRAIN-DUBAI-1992 (CP-5), SOMALIA-1978;
LOPATEV V.N., PATSONS J.M., ESPOSITO J.J.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ dat
EMBL; U87840; AAB94357.1; -.
EMBL; U87837; AAB94357.1; -.
EMBL; U87837; AAB94354.1; -.
HSSP; P25942; ICDE:
InterPro; IPRO01368; TNFR_C6.
Pfam; PF00020; TNFR_C6; 2.
PTODOM; PD000771; TNFR_C6; 1.
SMART; SM00208; TNFR_NGFR_1; 2.
PROSITE; PS00052; TNFR_NGFR_1; 2.
PROSITE; PS00050; TNFR_NGFR_2; 2.
SEQUENCE 349 AA; 38036 MW; EA412AEE86E090E4 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                O57284 PRELIMINARY; PRT; 349 AA.
O57284;
O1-JUN-1998 (TrEMBLrel. 06, Created)
O1-JUN-1998 (TrEMBLrel. 06, Last sequence update)
O1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

MEDLINE-21117110; PubMed-11172023;

Tone M., Tone Y., Fairchild P.J., Wykes M., Waldm
Tone M., Tone Y., Fairchild p.J., Wykes M., Waldm
Tregulation of CD40 function by its isoforms gene
"Regulation of CD40 function by its isoforms gene
alternative splitcing";
Proc. Natl. Acad. Sci. U.S. A. 98:1751-1756(2001).

EMBL; AJ401388; CAC29428 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41 SCKEDEYPVGSECCPKCSPGYRVKEACGELTGTVCEPCPPGTYIAHLNGLSKCLQCQMCD 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PNQGLRVKKEGTAESDTVCTCKEGQHCTSKD---CEACAQHTPCIPGFGVMEMATETTDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PAMGLRASRNCSRTENAVCGCSPGHFCIVQDGDHCAACRAYATSSPGQRVQKGGTESQDT 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCSDKQYLHDGQCCDLCQPGSRLTSHCTALEKTQCHPCDSGEFSAQWNREIRCHQHRHCE 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VCHPCPVGFFSNQSSLFEKCYPWTSCEDKNLEVLQK --- GTSQTNVICGLKSRMRALLVI 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LCQNCPPGTFSPNGTL-EECQHQTKCS----WLVTKAGAGTSSSHWVWWFLSGSLVIVIV 215
Score 266.5;
Pred. No. 2.3e
24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 268.5; DB 1
Pred. No. 9.5e-18;
                                                                                                                                     2.
2.
EA412AEE86E090E4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       stage;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Poxviridae; Chordopoxvirinae;
                         3e-17;
                                                     DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Waldmann H. generated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; 68
  76;
                                                                                                                                                                                                                                                                                                                                                                                                                 databases.
  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                     Length
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  15;
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  Gaps
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RESULT 057103 ID 057103 AC 05 DT 05 
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057098
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                 O57103 PRELIMINARY; PRT; 348 AA.
O57103;
O1-JUN-1998 (TrEMBLrel. 06, Created)
O1-JUN-1998 (TrEMBLrel. 06, Last sequence update)
O1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-SAUDI-M3;
LOPAREV V.N., PAISONS J.M.,
Submitted (JAN-1997) to the
EMBL; U87839; AAB94356.1; -.
HSSP; P25942; 1CDF.
                                                                             Orthopoxvirus.
                                                                                                                                                                                                            CRMB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00652; TNFR_NGFR_1; 2.
PROSITE; PS50050; TNFR_NGFR_2; 2.
SEQUENCE 349 AA; 37978 MW; 8630EFAED7A584B5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001368; TNFR_c6.

Pfam; PF00020; TNFR_c6; 2.

ProDom; PD000771; TNFR_c6; 1.

SMART; SM00208; TNFR; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            057098;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         057098
                                             NCBI_TaxID=10244;
                                                                                                                              Viruses;
                                                                                                                                                           Monkeypox virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Orthopoxvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Viruses; dsDNA viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Camelpox virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=28873;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21 LRLVLYLTFLGAPC-----YAPALPSCKEDEYPVGSECCPKCSPGYRVKEACGEL 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KGSSGCKACVSQTKCGIGYGV-SGHTSAGDVICSPCGLGTYSRTVSSADKCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QDGDHCAACRAYATSSPGQRVQKGGTESQDTLCQNCPPGTFSPN-GTLEECQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QDGDHCAACRAYATSSPGQRVQKGGTESQDTLCQNCPPGTFSPN-GTLEECQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MKSVLYSYILFLSCIIINGRDVTPYAPSNGKCKDNEYKRHNLCCLSCPPGTYASRLCDSK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KGSSGCKACVSQTKCGIGYGV-SGHTSAGDVICSPCGLGTYSRTVSSADKCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TNTQCTPCGSGTFTSRNNHLPACLSCNGRCD--SNQVETRSCNTTHNRICECSPGYYCIL 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGTVCEPCPPGTYIAHLNGLSKCLQCQ-MCDPAMGLRASRNCSRTENAVCGCSPGHFCIV 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MKSVLYSYILFLSCIIINGRDVTPYAPSNGKCKDNEYKRHNLCCLSCPPGTYASRLCDSK 60
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                                                                                                                  dsDNA viruses,
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33.1%;
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                                                                                                                      RNA stage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RNA stage;
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EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 266.5; DI
Pred. No. 2.3e-1
4; Mismatches
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                                                                                                                      Poxviridae; Chordopoxvirinae;
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Best Local
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057099;
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Loparev V.N., Parsons J.M., Esposito J.J.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; U87847; AAB94364.1; -
HSSP; P25942; ICDF.
InterPro; IPR001368; TMFR_C6.
Pfam; PF00020; TMFR_C6; 2.
ProDom; PD000771; TMFR_C6; 1.
SMART; SM00208; TMFR; 2.
                                                                                                                                                                                                                                                                                          STRAIN-SIERRA LEONE-1970 (70-0266);
Loparev V.N., Parsons J.M., Espositu
Submitted (JAN-1997) to the EMBL/Gen
EMBL; U87843; AAB94360.1; -.
HSSP; P25942; 1CDF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
                                                                                                                                                                                      PROSITE; PS00652; TNFR_NGFR_1; PROSITE; PS50050; TNFR_NGFR_2; SEQUENCE 349 AA; 38321 MW;
                                                                                                                                                                                                                                InterPro; IPR001368; TNFR_c6.
Pfam; PF00020; TNFR_c6; 2.
ProDom; PD000771; TNFR_c6; 1.
SMART; SM00208; TNFR; 2.
                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                               Orthopoxvirus
                                                                                                                                                                                                                                                                                                                                                                                                                          Viruses; dsDNA viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                                         Monkeypox virus.
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                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10244;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 LRLVLYLTFLGAPC-----YAPALPSCKEDEYPVGSECCPKCSPGYRVKEACGEL 70
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                                                                                     LRLVLYLTFLGAPC-----YAPALPSCKEDEYPVGSECCPKCSPGYRVKEACGEL 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KGSSGCRTCISKTKCGIGYGV-SGYTSTGDVICSPCGPGTYSHTVSSTDKCEPVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QDGDHCAACRAYATSSPGQRVQKGGTESQDTLCQNCPPGTFSPN-GTLEECQHQT 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGTVCEPCPPGTYIAHLNGLSKCLQCQ-MCDPAMGLRASRNCSRTENAVCGCSPGHFCIV 129
TNTQCTPCGSDTFTSHNNHLQACLSCNGRCD--SNQVETRSCNTTHNRICECSPGYYCLL
                           TGTVCEPCPPGTYIAHLNGLSKCLQCQ-MCDPAMGLRASRNCSRTENAVCGCSPGHFCIV 129
                                                         MRSVLYSYILFLSCIIINGRDIAPHAPSNGKCKDNEYRSRNLCCLSCPPGTYASRLCDSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TNTQCTPCGSDTFTSHNNHLQACLSCNGRCD--SNQVETRSCNTTHNRICECSPGYYCLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MRSALYSYILFLSCIIINGRDIAPHAPSNGKCKDNEYRSRNLCCLSCPPGTYASRLCDSK 60
                                                                                                                  Similarity
59; Conser
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                                                                                                                  Conservative
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                                                                                                                              16.8%;
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32.0%;
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                                                                                                                                                                                                                                                                                                                        EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                      Esposíto
                                                                                                               Score 265.5; DB 12,
Pred. No. 2.8e-17;
2; Mismatches 81;
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Pred. No. 2.8e-17;
                                                                                                                                                                                     2.
2.
FE449028CC933F57 CRC64;
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2.
34A5E668B27907B5 CRC64;
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                                                                                                                                                                                                                                                                                                                                      J.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              349
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                                                                                                                                            DB 12; Length 349;
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Best Local S
Matches 68
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057097;
01-JUN-1998 (TrEMBLrel. 0
01-JUN-1998 (TrEMBLrel. 0
01-JUN-2001 (TrEMBLrel. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2001 (
01-JUN-2001 (
01-JUN-2001 (
CD40 TYPE V )
EMBL;
         SEQUENCE FROM N.A.

STRAIN-IRAN (CP-1);

Loparev V.N., Parsons J.M., Esposito J.J.;

Submitted (JAN-1997) to the EMBL/GenBank/DDBJ

EMBL; U87838; AAB94355.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

MEDLINE-2117110; PubMed-11172023;

MEDLINE-2117110; PubMed-11172023;

Tone M., Tone Y., Fairchild P.J., Wykes M., Waldmann H.

"Regulation of CD40 function by its isoforms generated alternative spilicing.";

Proc. Natl. Acad. Sci. U.S.A. 98:1751-1756(2001).

EMBL; AJ401390; CAC29430.1; -.

EMBL; AJ401390; CAC29430.1; -.

SEQUENCE 260 AA; 28895 MW; 57A5BACE8CF2F546 CRC64;
                                                                                                                                                         01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-1001 (TrEMBLrel. 17, Last annotation update)
TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CD40.

CD40.

Mus musculus (Mouse).

Mus musculus (Mouse).

Metazoa; Chordata;

Metazoa; Rodentia;
                                                                                                     Orthopoxvirus
                                                                                                                Camelpox virus (strain CP-1).
Viruses; dsDNA viruses, no RN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
                                                                                        NCBI_TaxID=28873;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q99NEO;
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                                                                                                                                                                                                                                                                                                                                                                   LCQNCPPGTFSPNGTL-EECQHQTKCS----WLVTKAGAGTSSSHWVWWFLSGSLVIVIV 215
                                                                                                                                                                                                                                                                                                                                                  VCHPCPVGFFSNQSSLFEKCYPWTSCEDKNLEVLQK---GTSQTN----
                                                                                                                                                                                                                                                                                                                                                                                                                           PAMGLRASRNCSRTENAVCGCSPGHFCIVQDGDHCAACRAYATSSPGQRVQKGGTESQDT 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QDGDHCAACRAYATSSPGQRVQKGGTESQDTLCQNCPPGTFSPNGTLEECQHQTKCSWLV 189
                                                                                                                                                                                                                                                                                                                      CSTVGLIICVK-RRKPRGDVVKVIVSVQRKRQEAEGEATVIEALQAPPDVTTVAVEETI
                                                                                                                                                                                                                                                                                                                                                                                                        PNQGLRVKKEGTAESDTVCTCKEGQHCTSKD---CEACAQHTPCIPGFGVMEMATETTDT 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCSDKQYLHDGQCCDLCQPGSRLTSHCTALEKTQCHPCDSGEFSAQWNREIRCHQHRHCE 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SCKEDEYPVGSECCPKCSPGYRVKEACGELTGTVCEPCPPGTYIAHLNGLSKCLQCQMCD 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KGALGCRTCISKTKCGIGYGV-SGYTSTGDVICSPCGPGTYS-----HTVSSTDKCEPVV 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68;
                                                                                                                                                                                                                                                                                               ----VICEKVVKKPKDN--EMLPPAARRQDPQEME-----DYPGHNTAAPVQETL
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1 (TrEMBLrel.
1 (TrEMBLrel.
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17,
17,
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                                                                                                                   RNA stage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 265; DB 11;
Pred. No. 2.3e-17;
4; Mismatches 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                              349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             260
                                                                                                                   Poxviridae; Chordopoxvirinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95;
                       databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                               227
                                                                                                                                                                                                                                                                                                                         273
                                                                                                                                                                                                                                                                                                                                                   183
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Best Local Similarity
Matches 57; Conserv
                                                                                                                                                                                                                                        InterPro; IPR001368; TNFR_c6.

Pfam; PF00020; TNFR_c6; 2.

ProDom; PD000771; TNFR_c6; 1.

SMART; SM00208; TNFR; 3

PROSITE; PS00652; TNFR_NGFR_1; 1

PROSITE; PS500650; TNFR_NGFR_2; 2

SEQUENCE 349 AA; 37944 MW; 8
                                                                                                                                                                                                                                                                                                                                          HSSP; P25942; 1CDF
 119
                           130
                                                       61
                                                                                 71
                                                                                                                                         21
                                                                                                                             LRLVLYLTFLGAPC-----YAPALPSCKEDEYPVGSECCPKCSPGYRVKEACGEL
                                                                      TGTVCEPCPPGTYIAHLNGLSKCLQCQ-MCDPAMGLRASRNCSRTENAVCGCSPGHFCIV 129
                                                                                                               MKSVLYSYILFLSCIIINGRDVTPYAPSNGKCKDNEYKRHNLCCLSCPPGTYASRLCDSK 60
KGSSGCKACVSQTKCGIGYGV-SGHTSAGDVICSPCGLGTYSRTVSSADKCE
                          QDGDHCAACRAYATSSPGQRVQKGGTESQDTLCQNCPPGTFSPN-GTLEECQ 180
                                                       TNTQCTPCGSGTLTSRNNHLPACLSCNGRCD--SNQVETRSCNTTHNRICECSPGYYCIL
                                                                                                                                                                     Conservative
                                                                                                                                                                                  16.6%;
                                                                                                                                                                   23;
                                                                                                                                                                  Score 262.5;
Pred. No. 5.4e
23; Mismatches
                                                                                                                                                                                                                                        1.
2.
829EA54ED4C60455 CRC64;
                                                                                                                                                               5.4e-17;
77;
                                                                                                                                                                     Indels
                                                                                                                                                                                               Length 349;
169
                                                                                                                                                                   15;
                                                                                                                                                                   Gaps
                                                       118
                                                                                                                                         70
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Search completed: January 24, 2002, 16:25:00 Job time: 195 sec

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